STIC-Biotech/ChemLib

From:

Sent:

Jiang, Dong Monday, July 16, 2001 4:11 PM STIC-Biotech/ChemLib SN09/488,728

To: Subject:

Please search 1 to 322 of SEQ ID NO:2, and 1 to 320 of SEQ ID NO:4

-issued

-commercial

Please send results on paper to Dong Jiang in 10B-01 (mail stop CM1-10C01). Thank you very much.

Dong Jiang (78243) 703-305-1345 U.S. Patent and Trademark Office Art Unit 1646

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Access DB#<u>468/</u>3

SEARCH REQUEST FORM

Scientific and Technical Information Center

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Inventors (please provide it	in names).			
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SEQUENCE FROM N.A.
TISSUE-THYMOMA EL4;
MEDLINE-96111968; PubMed-8777726;
Yao Z., Fanslow W.C., Seldin M.F., RC
Comeau M.R., Cohen J.I., Spriggs M.K.
"Herpesvirus Saimiri encodes a new cy
Inmunity 3:811-821(1995).
EMBL: U31993; AAC52357.1;
MCD; MGI:107399; Il17r,
SEQUENCE 864 AA; 97807 MW; 343FD;
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Mus musculus (Mouse).
Mus musculus (Mouse).
Theria; Rodentia; Cr
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Sciurognathi; Muridae; Murinae; Mus.
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Oncogene 19:2098-2109(2000).
EMBL; AF208110; AAF86051.1; -.
                                    MEDLINE=20273223; PubMed=10815801; Tian E., Sawyer J.R., Largaespada Shaughnessy J.D. Jr., Largaespada "Evi27 encodes a novel membrane pr
                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
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Q9NRM6;
01-OCT-2000 (TrEMBLrel. 15, Created)
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MEDILINE=20317118; PubMed=10749887;
Shi Y., Ullrich S.J., Zhang J., Connolly K., Grzegorzewski K.J.,
Barber M.C., Wang W., Wathen K., Hodge V., Fisher C.L., Olsen H.,
Ruben S.M., Knyazev I., Cho Y.H., Kao V., Wilkinson K.A.,
Carrell J.A., Ebner R.;
A novel cytokine receptor-ligand pair. Identification, molecular Characterization, and in vivo immunomodulatory activity.";
EMBL; AF212365; AAF78776.1; -.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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8; Mismatches
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SIGNAL
CHAIN
SEQUENCE
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                                                          B
                                                                                                                                        Query Match
Best Local S
Matches 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 LGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDDSWIHPRNLTPSSPKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
11-17 RECEPTOR HOMOLOG PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9JIP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSLVLISLAALC------RSAVPREPTVQC--GSETGPSPEWMLQHDLIPGDLRD 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20273223; PubMed=10815801;
Tian E., Sawyer J.R., Largaespada D.A., Jenkins N.A.,
Shaughnessy J.D. Jr.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                      oncogene 19:2098-2109(2000).
                                                                                                                                                                                                                                                                                                                                                                 receptor.
                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVL-QLNTNERLCYRFE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARM 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRVEPVTTSVATGDYSILMNVSWVLRADASIRLLKATKICVTGKSNEQSYSCVRCNYTEA 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHMENHSCFEHMH 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 Similarity
82; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QVFEPHQKKQTRASVVIPVTGDSEGA---TVQLTPYFPTCGSDCIRHKGTVVLCPQ---T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KYKKKCVKAGSLWDPNITACKKNEETVEVNFTTTPLGNRYMALI-----QHSTIIGFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEPIP 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIPAPRPEEFHORSNYTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT-VSCPEMPDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GVPFP 279
                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Receptor.
                                                                                                      19
                        79
                                                                                                LLLLLGVLAPGGASLRLLDHRALVCSOPGLNCTVKNSTCLDDSWIHPRNLTPSSPKDLQI 78
                                                                                                                                                                                                                                                                                                                         AF208108; AAF86049.1; -.
                                                            HILVELITA---ASC----RSALPREPTIQC--GSETGPSPEWMVQHTLTPGGLRDLQV
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QLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVL-QLNTNERLCVRFE----FLS 133
                                                                                                                                                                                                                                                                                                                                                                                   encodes a novel membrane protein with homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                         Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                   499
                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                          91
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55918 MW;
                                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.1%; Score 284; DB 4;
26.9%; Pred. No. 1.2e-19;
                                                                                                                                                                                                                                                      8 P
499 I
; 55617 MW;
                                                                                                                                                              15.4%; Score 272.5; DB 11;
27.6%; pred. No. 1.6e-18;
27.6%; mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
IL-17 RECEPTOR HOMOLOG.
; 9C84A63EC123FF17 CRC64;
                                                                                                                                                          45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                          POTENTIAL.
IL-17 RECEPTOR HOMOLOG.
C66440430E3C31F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     499
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                                                                                                                                                                                                             DB 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130
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                                                                                                                                                                                Gaps
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Q9JIP2
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AC Q1
DT 0
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Best Local Similarity 26.8
Matches 60; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
TRUNCATED IL-17 RECEPTOR HOMOLOG PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9NRM5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                308
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. Denkins N.A., Cop. MEDLINE=20273223; PubMed=10815801; Tian E., Sawyer J.R., Largaespada D.A., Jenkins N.A., Cop. Shaughnessy J.D. Jr.; Shaughnessy J.D. Jr.; Eyi27 encodes a novel membrane protein with homology to "Eyi27 encodes a novel membrane protein with homology to
                                                                                                                                                                                                                                                                                                                                                     receptor.";
Oncogene 19:2098-2109(2000).
EMBL: AF208111; AAF86052.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                 Signal; Receptor.
                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARWKVT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELVKTSVAAEEFSILMNISWILRADASIRLLKATKICVSGKNNMNSYSCVRCNYTEAFQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPCMSSGSLWDPNITVETLEAHOLRVSFTLWNESTHYOILL----TSFPHMENHSCFEH 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MHHIPAPRPEEFHORSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT-VSCPEMP 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
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KQCTEAGSLMDPDITACKKNEKMVEVNETTNPLGNRYTILIQRDTTLGESRVLENKLMRT
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 Q9JIP2;
01-OCT-2000
                       Q9JIP2
                                                                                                                                              131
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                                                                                                  191
                                                                                                                        108
                                                                              168
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                                                                                                                                                                  48
                                                                                                                                                                                                             ب
                                                                                                                                                                                                           MSLVLISLAALC-----RSAVPREPTVQC--GSETGPSPEWMLQHDLIPGDLRD
                                                                                                                                                                                                                                 LGLLLLLLGVLAPGGASLRLLDHRALVCSOPGLNCTVKNSTCLDDSWIHPRNLTPSSPKD
                                                                                                                                                                                     LQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVL-QLNTNERLCVRFE---- 130
                                                                                                                                          FLSKLRHHHRRWRFTESHFVVDDDQEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARM 190
                                                                                                                                                                LRVEPVTTSVATGDYSTLMNVSWYLRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEA 107
                                                                                                                      KYTTPCMSSGSLMDPNITVETLEAHOLRYSFTLMNESTHYQILL 234
                                                                             KYKKKCVKAGSLWDPNITACKKNEETVEVNFTTTPLGNRYMALI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                               14
288 AA;
    (TrEMBLrel. 15,
                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -DYMPLW
                                                                                                                                                                                                                                                                                                                  13
288
7
31773 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----GAV---VOLTPYLHTCGNDCIRREGTVVLCSE-
                                                                                                                                                                                                                                                                      12.5%; Score 220;
26.8%; pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291
                                                                                                                                                                                                                                                                37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                     POTENTIAL.
TRUNCATED IL-17 REC
; CD8EB2C0C235FBFB
            Created)
                                   PRT;
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                                                                                                                                                                                                                                                                                                                         IL-17 RECEPTOR HOMOLOG
0C235FBFB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
                                     218
                                                                                                                                                                                                                                                                                DB 4;
                                                                                                                                                                                                                                                                       109;
                                                                                                                                                                                                                                                                                            Length 288;
                                                                                                                                                                                                                                                                        Indels
                                                                                              211
                                                                                                                                                                                                                                                                                                                                                                                                                            Copeland N.G
                                                                                                                                                                                                                                                                                                                                                                                                           the
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                                                                                                                                                                                                                                                                             Gaps
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RESULT
061339
ID 066
AC 066
DT 010
DT 011
DT 011
DT 011
DT 02
GN T2
GN T
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061939; OTTEMBLE 07, C
01-NOV-1999 (TEMBLE 12, L
01-MAR-2001 (TEMBLE 116, L
STRAIN-BRISTOL N2;
Taich A., Gattung S., Le T.T.;
The sequence of C. elegans cosmid T24A6.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                          "Genome sequence of the nematode C. elegans: a plinvestigating biology, The C. elegans Sequencing Science 282:2012-2018(1998).
                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=BRISTOL N2; MEDLINE=99069613;
                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
Bukaryota; Metazoa; Nematoda; Chromadorea
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
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                                                                                                                                                                                                                         None;
                                                                                                                                                                                                                                                                                                                                                                                               T24A6.8 PROTEIN.
T24A6.8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 OTRPSGGKWTFSYVGFPVELSTLYLISAHNIPNANMNEDSPSLSVNFTSPGCTRENTEVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 KLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARMKVT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal; Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002259; -. ProDom; PD005103; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shaughnessy J.D. Jr.; "Evi27 encodes a novel membrane protein with homology to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=20273223; PubMed=10815801;
Tian E., Sawyer J.R., Largaespada D.A., Jenkins N.A.,
Shaughnessy J.D. Jr.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oncogene 19:2098-2109(2000).
EMBL; AF208109; AAF86050.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Eukaryota; Metheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
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IL-17 RECEPTOR HOMOLOG SHORT ISOFORM PRECURSOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171
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                                                                                                                                                                                                                   PubMed=9851916;
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218
23855 <sub>1</sub>
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                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence up
Last annotation
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Pred. No. 1.6e-08;
Mismatches 83;
                                                                                                                                                                                                                                                                                                                               Chromadorea;
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IL-17 RECEPTOR HOMOLOG SHORT ISOFORM; E17C154C824E1F0B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              398
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Murinae; Mus.
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01-MAY-2000 (TrEMBLrel 13, Las
01-MAR-2001 (TrEMBLrel 16, Las
CAP BINDING PROTEIN 80
CBP80 OR EG:84H4.3 OR CG7035.
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                                                                                    Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
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Best Local S
                                                         STRAIN-OREGON R; TISSUE-IMAGINAL DISC;
Lewis J.D.;
                                                                              SEQUENCE FROM
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InterPro; IPR001628;
Pfam; PF00104; hormone_rec; 2.
Pfam; PF00105; zf-C4; 2.
PRINTS; PR00047; STROIDEINGER.
SMART; SM00430; HOLI; 1.
SMART; SM00399; ZnF_C4; 1.
DNA-binding; Nuclear protein; Re
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                                                                                                                                                                                                                                                                                                                        273
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SEQUENCE 3
                                                                                                                                                                                                                                                                                                                                                                                                                                 109
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SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston R.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELJULAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL: AF068713; AAC17795.2; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 KCMYCVRPAHGYHCDVATCKGCKTFFRRMCLLRGEIKCSTSGDCYDLEKRNSPLLRCRPC 92
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                                                                                                                                                                                                                                                                                       LWNESTHYQILLTSFPHMENHS 244
                                                                                                                                                                                                                                                                     IEKERHHYSNILLKY-CLQNYS
                                                                                                                                                                                                                                                                                                         NEPHYCAHTVPFGPMKRIKIQFNEFLLLKILFVC
                                                                                                                                                                                                                                                                                                                      -DPNH------QSKNFLVPDCDHARMKVTTPCMSSGSLWDDNITVETLEAHQLRVSFT
                                                                                                                                                                                                                                                                                                                                          MTAVEYTKTFSFFHDLSFQDQINLLKHVVIGLANFNTTYYTLKNKFDDLRQPDGTQRPGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----LTPSSPKDLQ1------QLHFAHTQ-QGDLFPVAHIEWTLQTDASILY---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity 20.5
66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        -LEGAELSVLOLNINER-----LCVRFEFLSKLRH------HHRRWRF---
                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 398 AA;
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20.5%;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 97.5; DB 5;
Pred. No. 0.19;
8; Mismatches 89
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Best Local Similarity
Matches 56; Conserv
RA ADTII J.K., AGDAYANI A., ANI H.-U., MULLEWS-TLAULINOUL, C., DEASLEY E.M.,
RA BALLEW R.M., BASCA A., BASCANDA A., BAYBAKTATOGUL L., Beasley E.M.,
RA BESON K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA BUTTIS K.C., BUSAM D.A., BULLET H., Cadieu E., Center A., Chandra I.,
RA BUTTIS K.C., BUSAM D.A., BUTLET H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Duer S., Fleischmann W.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Pollard J., Puri V., Reese M.G.,
RA Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,
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Ephydroidea; Dro
NCBI_TaxID=7227;
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE003431; AAF45970.1; -.
EMBL; AL031766; CAA21136.1; -.
FlyBase; FBgn0022942; Cbp80.
SEQUENCE 800 AA; 93226 MW;
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FERTAZ C., Vidal S., Brun C., Bucheton A., Dem
"Sequencing the distal X chromosome of Drosoph
"Submitted (SEP-1998) to the EMBL/GenBank/DDBJ
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                                                                                                                                                                                                01-MAR-2001 (TERMBLEEL 16, Cree 01-MAR-2001 (TERMBLEEL 116, Last 01-MAR-2001 (TERMBLEEL 16, Last HYPOTHETICAL 134.3 KDA PROTEIN.
                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                              190
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                                                                                                                                                                                     DKFZP434H1220.
                                                  Ottenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AL136800; CAB66734.1;
                                                                                                                                                                                                                                                                                                                                                                                    294
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                            Hypothetical SEQUENCE 1:
                                                                                                                                 NCBI_TaxID=9606
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                                                                                                                                                                                                                                                                                                                                                                                                                                      AQIRKLRQDNWAEKHIPRPYLVFDSILCEALQHNLPTIVP--PPHHDNFEYPMPWVVY-R
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Query Match

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93;

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RESULT SOULDS ID COPE OF COPE 
                                                                                                                                                                                                                                                                                                             Matches
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Best Local
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Q9ULD3;
01-MAY-2000
01-MAY-2000
                                                                                   118
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                  "Prediction of the coding sequences of unidentified human genes. The complete sequences of 100 new cDNA clones from brain which co for large proteins in vitro.";

EMBL; AB033113; BAA86601.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel 13, 01-MAY-2000 (TrEMBLrel 13, 01-MAY-2000 (TrEMBLrel 13,
                                                                                                                                                                                                                    709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20039619; PubMed=10574462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KIAA1287
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                                                                                                                                                                         73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1010 NIAKLVHFQGYPCELLPLTVAGIPSMHICLDFIP 1043
                                                                                                                                                                                                                                                                29
                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       957
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                               Q-----LNT--NERLCY------RFEFLSKLRHHHRRWRFTFSHFVYDP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   704
                                                                                                  PKQLQEAFSAVPVNHTQVMQIIEHLTLLSASELIPYAEV---LTSNMSQLLNSGVPRRIL
                                                                                                                                                                                                                              GGLHSALL--RLLATNYPHL------CIVDDWICEEEITGTDALLRRMLLTNNAKNHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VNPDSLLRNVQSVITTSAPNKGMEEGEDNLLCNLREVQ------CLICCLLHQMYIADP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APEVTRE----ELKNALLAAQDSAAVQILL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHMENHSCFEHMH1IPAPRPEEFHQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DQR----VHRCP-PLMD-ITLHMLNGYLLASKAYLSAHLKETEQDRPSQNNTIGLVGQTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QTVNKLWMVLNTVMPRRLWVWTVNALQPSIKFV-----RQQKYTQNDLMIDPLIVLRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q------LNT--NERLCV------RFEFLSKLRHHHRRWRFTFSHFVVDP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PKQLQEAFSAVPVNHTQVMQIIEHLTLLSASELIPYAEV---LTSNMSQLLNSGVPRRIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PKDL-----QIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVL 117
                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGLHSALL--RLLATNYPHL-----CIVDDWICEEEITGTDALLRRMLLTNNAKNHS 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGASLRLLDHRALVCSQPGLNCTVKNSTCLDDSWIHPRNLTPS-----------
                                                                                                                                                                                                                                                                                                                                                                                                               1209 AA;
                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                       5.3%;
                                                                                                                                                                                                                                                                                                                                                                                                          134941 MW;
                                                                                                                                             ---QIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVL
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                                                                                                                                                                                                                                                                                               36;
                                                                                                                                                                                                                                                                                                           Score 93; DB /
Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1.8; 6; Mismatches
                                                                                                                                                                                                                                                                                     Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                 BF44BD99F71A37B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1209
                                                                                                                                                                                                                                                                                                                                DB 4; Length 1209;
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                                                                                                                                                                                                                                                                                   Indels 158;
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                       RA Adams M.D. (Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., RA Amanatides P.G., Kortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Ballew R.R., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Ballew R.M., Baster E.G., Helt G., Welson C.R., Miklos G.L.G., RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., RA Ballew R.M., Basu A., Baxendale J., Brokstein P., Botshakov S., Burtis H.J., Andrews-Pfannkoch C., Baldwin D., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Botshakov S., W., Berman B.P., Welson P. Brottier P., Botchan M.R., Bouck J., Brokstein P., Brottier P., Botchan M.R., Bouck J., Brokstein P., Brottier P., Cadieu E., Center A., Chandra I., RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Glasser K., RA Harris M., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Harris N., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Harris M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Moyland T.J., Wei M.-H., Diegwam C., RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Lai Z., Liang Y., Liin X., Ra Harris M., Murphy B., Murphy B., McPherson D., McPherson D., Ra McKulov G., Milshina N.V., Mobarry C., Moris J., Moshrefi A., Ra Autil J., Martin J., Martin J., Martin J., Walley D.M., Nelson D.L., Reader J.C., Scheeler F., Shen H., Sh
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Q9VGY6
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Q9VGY6;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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01-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -VHRCP-PLMD-ITLHMLNGYLLASKAYLSAHLKETEQDRPSQNNTIGLVGQTD 922
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13,
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Best Local :
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InterPro; IPR003600; ...
Pfam; PF00047; ig; 3
PROSITE; PS00290; IG_MHC; U
SMART; SM00410; IG_like; 11.
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation updat
MACROPHAGE MEMBRANE PROTEIN MFP150.
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=FISHER 344;
MEDLINE=98449911; pubMed=9774638;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
NCBI_TaxID=10116;
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EMBL: U62328; AAC68478.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
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LEGAELSVLQLNTNER-----LCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYE----V
                                                                                                              PPSAVP---GPLLGLLLLLLGYLAPG--GASLRLLDHRALVCSQPG----LNCTVKNSTC
                                                         LDDSWIHPRNLTPSSPKDLQIQLHFAHTQQ------
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| 79; Conserv
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                              -SLTPVGP----IKWFKGEGQNRSPIYSFIGGEHFP----RITNVSDAT--K
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Pred. No. 2;
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Pred. No.
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Q9SJR7;
Q1-MAY-2000
01-MAY-2000
01-MAR-2001
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Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of chromosome II of Arabidopsis thaliana.";
Nature 402:761-768(1999).
EMBL; A0006919; AAPI8663.1; -.
InterPro; IPR003592; -.
SMART; SM00370; LRR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; S
Magnoliophyta; eddicotyledons; core eudicots; Rosidae;
Brassicales; Brassicaceae; Arabidopsis.
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                        HIPAPRPEEFHORSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSATVSCPEMP 307
                                                                                                                                                                      ----QLNEASLL----LSILPNSYFANLRWRKSLESFLKNPDDDERHQEQISHRTLPILSF
                                                                                       WNE
                                                                                                               E---SVKEIDISKCQRLDYKVVIKCFSKSFPSLRKLRAAYLLNIKVSTL--LELLLNFRE 322
                                                                                                                                          DPNHQSKNFLVPDCEHARMKVTTPCMSSG-----SLWDPNITVETLEAHQLRVSFTL
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TLHMSKCEGISETSLLNLITHS
                                                      LTEVDLTVDVSPIIPVQASVFYSGQVCYTSFSENSILALCATISMTNEHMDINSVASNLQ
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Search completed: July 17, 2001, 11:20:43 Job time: 162 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.
 Length DB
   TBXT_CHICK
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T2D2_DROME
AMEP_BOVIN
PYR1_SQUAC
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       p28668 drosophila
p4439 haemophilus
p04172 homo sapien
q09898 schizosacch
p57678 homo sapien
p51526 anas platyr
p97760 mus musculu
p35852 lactobacill
p11279 homo sapien
p19387 homo sapien
p19387 homo sapien
p79778 gallus gall
q02381 hepatitis a
p52022 vibrio chol
p30855 escherichia
q04833 caenorhabdi
q09813 rattus norv
q24325 drosophila
p00978 bos taurus
q01437 squalus aca
q54917 mus musculu
p38494 homo sapien
p13473 homo sapien
p10643 homo sapien
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p00533 homo sapien
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132; Li P.W., Evans C.A., Li P.W., Hoskins R. Robert S., Kandari D., Robert L.B. L. Dayenport L.B. L. Dayenport L.B. L. Dayenport L.B. L. Dayenscha S., Li L. Dayenscha S., Li L. Gu Z., Genbart W. L. Dugan-Rocha S., H., Gu Z., Genbart W. L. Dugan-Rocha S., R. J. Hernandez J. H., Gu Z., Guan P. H., Gu Z., Kennison H., Ke Z., Kennison H., Ke Z., Kennison H., Ke Z., Kennison H., Ke Z., Kennison H., Li J., Li Z., Li Li Li Li Z., Li L	PRT; 184 AA. ated) it sequence update) it annotation update) 8817. (Fruit fly). ("Fruit fly). ("Topoda; Tracheata; Hexapoda; In "Topoda; Diptera; Brachycera ae; Drosophila.	AGLU_SPIOL ACON_MYCAV HIRA_MOUSE EGFR_MOUSE EGFR_MOUSE VGLE_SVVL VGLE_SVVL VGLE_SVVD RRPL_SV5 RRPL_SV5 RRPL_SV5 RRPL_SV5 RRPL_SV5 RRPL_SV5 RRPL_SV5 ALIGNMENTS
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P18570;
01-NOV-1990
                                                                                                DOMAIN
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"Identification of the gene encoding
                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90357782; PubMed=2167559;
                                                                                                                                                                                                                                                                                                                                                                                                  Rotavirus (group B / strain ADRV)
Viruses; dsRNA viruses; Reoviridae
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15-JUL-1999
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                                                                                                                                                A37080;
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PRECURSOR (OUTER SHELL GLYCOPROTEIN).
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27.4%;
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                               e; Glycoprotein; Signal.

POTENTIAL.
GLYCOPROTEIN VP7.
CHARGED, HYDROPHILIC REGION.
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
MW; OBEIOCDICBB2AFB3 CRC64;
   Score 88.5;
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Pred. No. 0.42;
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of the ADRV
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segment 9
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RESULT 3
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InterPro; IFR000822; -. Pram: PF00096; zf-C2H2; 7.
Pfam: PF00096; zf-C2H2; 7.
PRINTS; PR00048; ZINC_FINGER_C2H2_1; 7.
PROSITE; PS00028; ZINC_FINGER_C2H2_2; 7.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 7.
Developmental protein; Zinc_finger; Metal-binding; DNA-binding; Nuclear protein; Transcription regulation; Repeat.
ZN_FING 432 454 C2H2-TYPE.
ZN_FING 432 454 C2H2-TYPE.
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                                                                                                                                  HSSP; P04002; 1WFA.
FlyBase; FBgn0013137;
                                                                                                                                                                EMBL; 227444; CAA81800.1;
PIR; S42748; S42748.
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                                                                                                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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MEDIJINE-9413659; PubMed-7905822;

Kuehnlein R.P., Frommer G., Friedrich M., Gonzalez-Gaitan M.,

Wagner-Bernholz J.F., Gehring W.J., Jaeckle H., Schuh R.;

"Spalt encodes an evolutionarily conserved zinc finger protein of novel structure which provides homeotic gene function in the head and tail region of the Drosophila embryo.";

EMBO J. 13:188-179(1949).
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01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation updat
HOMEOTIC PROTEIN SPALT-MAJOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila virilis (Fruit fly)
Eukaryota; Metazoa; Arthropoda;
Pterygota; Neoptera; Endopterygo
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                                                                                                                                                                                                                                                                                                                                      FUNCTION: REQUIRED FOR THE ESTABLISHMENT OF THE POSTERIOR-MOS HEAD AND THE ANTERIOR-MOST TAIL SEGMENTS OF THE EMBRYO, PROBA FUNCTION AS A TRANSCRIPTIONAL REGULATOR. COULD REPRESS THE TRANSCRIPTION OF THE TSH GENE.

TRANSCRIPTION OF THE TSH GENE.
SUBCELULAR LOCATION: NUCLEAR (PROBABLE).

DEVELOPMENTAL STAGE: FIRST EXPRESSED AT BLASTODERM STAGE AND LATTER IN RESTRICTED AERAS OF THE EMBRYONIC NERVOUS SYSTEM AS
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Endopterygota; Diptera; Brachycera; Musc
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P00533; P06268; Q14225;
P1-JUL-1986 (Rel. 01, Created)
O1-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
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                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE-84219729; PubMed-6328312;

MEDLINE-84219729; PubMed-6328312;

Ullrich A., Coussens L., Hayflick J.S., Dull T.J., Gray A., Tam A.F.

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Mayes E.L.V., Whittle N., Waterfield M.D., Seeburg and aberrant

"Human epidermal growth factor receptor cDNA sequence and aberrant

Compression of the amplified gene in A431 epidermoid carcinoma cells

Mature 309:418-425(1984).
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Mammalia; Eutheria;
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 SEQUENCE OF 150-962 FROM N.A.
MEDLINE-84245835; PubMed=6330563;
Xu Y., Ishii S., Clark A.J.L., Su.
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                                                                                                                                                                                SEQUENCE OF 713-924 FROM N.A. MEDLINE-84196372; PubMed=6326261;
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"Human epidermal growth factor receptor cDNA is homologous variety of RNAs overproduced in A431 carcinoma cells."; nature 309:806-810(1984).
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MEDLINE-85046483; PubMed-6093780;
Simmen F.A., Gope M.L., Schulz T.Z.,
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O'Malley B.W.;
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"Contributory effects of de novo transcription and "ranscript termination in the regulation of human transcript termination in the regulation of factor receptor proto-oncogene RNA synthesis.";
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"ATP-stimulated interaction between and supercoiled DNA.";
Nature 309:270-273(1984).
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MEDLINE-84191554; PubMed-6325948;
Mroczkowski B., Mosig G., Cohen S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (SEP-1997)
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                                                                                                                                U. Rev. 'Biochem. 56:881-914(1987).
FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL SIGNAL OF EGF,
AND ALSO OF TGF-ALPHA, AMPHIREGULIN, HEPARIN-BINDING EGF, GP30 AND
VACCINIA VIRUS GROWTH FACTOR:
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                                                                                                                                                                                                                                                                                                                                                                                                     ĀΑ;
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AT SIMILARITY

PHOSPHORYLATION (B. PHOSPHORYLATION (AUTO PHOSPHORYLATION (BUCNAC...) (POTALINKED (GLCNAC...) (POTALIN
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                             Mismatches
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D8A2A50B4EFB6ED2 CRC64;
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No.
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1.3;
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                                                                                                                                                                                                                                                                                Length 1210;
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.) (POTENTIAL).
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-LHFAHTQQGD
                                                                                                                                                                                                                   118;
                                                                                                                                                                                                         Gaps
                                                                                       836
                                                                                                                                                   64
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RX MEDLINE-20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,

RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Kopers Y.-H.C., Blazej R.G., Champo Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champo M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Burtls K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
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                                                                                                                                                                                                                                                                                                                                Cerini C., Semeriva M., Gratecos D.;
"Evolution of the aminoacyl-tRNA synthetase family and the organization of the Drosophila glutamyl-prolyl-tRNA synthetase Intron/exon structure of the gene, control of expression of the mRNAs, selective advantage of the multienzyme complex.";

Eur. J. Biochem. 244:176-185(1997).
                                                                                                                                                                                                                                                                                                   STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE=92097547; PubMed=1756734;

Cerini C., Kerjan P., Astler M., Gratecos D., M.

"A component of the multisynthetase complex is aminoacyl-trna synthetase.";

EMBO J: 10:4267-4277(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97217441; PubMed=9063462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P28668; 09VCF5,

01-DEC-1992 (Rel. 24, Created)

01-DEC-1992 (Rel. 24, Last sequence update)

01-OCT-2000 (Rel. 40, Last sequence update)

01-OCT-2000 (Rel. 40, Last annotation update)

BIFUNCTIONAL AMINACYL-TRNA SYNTHETASE (INCLUDES: GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE-TRNA LIGASE); PROLYL-TRNA SYNTHETASE (EC 6.1.1.15) (PROLINE-TRNA LIGASE)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-OREGON-R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GALTEDSIDDTFLPVPEYINQSVPKRPAGSVQNPVYHNQPLNPAPSRDPHYQDPHSTAV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EYLIPOOGFFSSPSTSRTPLLSSLSATSNNSTVACIDRNGLOSCPIKEDSFLORYSSDPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -TLWNESTHYQILLT-----SFPHMENHSCFEHMHH----IPAPRPEEFHORSNVTLTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VWSYGVTVWELMTFGSKPYDGIPASEISSI-LEKGERLPQPPICTIDVYMIMVKCWMIDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -GNPEYLNTVQP---TCVNSTFDSPAHWAQKGSHQISLDNPDVQQDFFP 1178
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a; Brachycera; Muscomorpha;
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s a multifunctional
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RA Dodson K., Doup L.E., Downes M., Duyaur, D., Dong F., Erleschmann W., RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeyman C., RA Liu X., Mattel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Ra Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.R., RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.L., RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson N.L., RA Nelson D.R., Nelson K.A., Nubarry C., Morris J., Moshrefi A., RA Nelson D.R., Nelson K.A., Mishina N.V., Mobarry C., McTele J.M., Pacleb J.M., RA Nelson D.R., Saunders R.D.C., Scheeler F., Shen H., RA Ra Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RA Shue B.C., Spradling A.C., Stapleton M., Strong R., Sun E., Shen B.C., Spradling A.C., Stapleton M., Strong R., Sun E., Shen B.C., Spradling A.C., Stapleton M., Strong R., Wang A.H., Wang A.H., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., RA Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., RA Yellans S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., RA Yellans S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., RA Yellans S.M., Woodage T., John M., Zhou X., Zhu X., Smith H.O., RA Zheng X.H., Zhong F.N., Zhou X., Zhu X., Smith H.O., RA Zheng X.H., Zhong F.N., Zhou X., Zhu X., Smith H.O., RA Zheng X.H., Zhong G., Zheng L., CARALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU) = AMP + CCC - TARALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU).
                                                                                PlyBase; FB900005674, Aats-glupro.

FlyBase; FB900005674

Interpro; IPR000738;

Interpro; IPR000924;

Interpro; IPR000216;

Interpro; IPR00216;

Interpro; IPR00216;

Interpro; IPR002316;

Interpro; IPR002314;

Interpro; IPR002314;

Interpro; IPR002316;

Interpro; IPR002314;

Interpro; IPR002316;

Interpro; IPR002314;

Interpro; IPR002316;

INTERPO0458; WHEP-TRS; 6.

PFAm; PF00587; TRNA-SYNTHGLU,

PFAm; PF00587; TRNA-SYNTHGLU,

PRINTS; PR01046; TRNA-SYNTHGLU,

PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.

PROSITE; PS00178; AA_TRNA_LIGASE_II_1; FAP

PROSITE; PS00339; AA_TRNA_LIGASE_II_2; FAP

PROSITE; PS00762; WHEP_TRS; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long use by and for commercial modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M74104; AAA28594.1; -. EMBL; U59923; AAC47469.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE003745; AAF56211.1; ..
       Multifunctional enzyme; Repeat Multifunctional 754 GI DOMAIN 755 800 WI
                                                               minoacyl-tRNA synthetase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: CONTAINS 6 "WHEP-TRS" DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             S18644; S18644.
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                                                                                Protein biosynthesis; Ligase; ATP-binding;
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                  GLUTAMYL-TRNA SYNTHETASE. WHEP-TRS 1.
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                                                                                                                                                                                                                                                                                                                                                           32 SLRLLDHRALVCSQPGLNCTVKNSTCLDDSWIHPRNLTPSSP------KDLQIQ--
                                                                                                                                                                                                                                                                                                                                                                                      Local
                                     p44398;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
XYLOSE ISOMERASE (EC 5.3.1.5).
XYLA OR HIII12.
XYLA OR HIII112.
Haemophilus influenzae.
                                                                                                                                                                                                                                            193
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                                                                                                XYLA_HAEIN
                             Bacteria; Proteobacteria;
                                                                                                                                        361 TIYRCKNEP 369
                                                                                                                                                          299
                                                                                                                                                                                                                                                                                                                           LHFAHTQQGDLFPVAHIEWTLQTDAS----ILYLEGAELSVLQLNTNERLCVRFEFLSK- 134
                                                                                                                                                                                                                                                                                                                                             SLQFPDNRLLVCH----
                                                                                                                                                                                                                                                                                                            LSFSLICEDD-----ISWALSFLTSPLPPVTYLVANKLTIADFALFNEMHSKYEFLAAK 137
                                                                                                                                                                                                                                           FVDLPGAEMGKVVVRFPPEASGYLHIGHAKAALLNQYYALVCQGTLIMRFDDTNPAKETV
                                                                                                                                                                                                                                                           NFLVPDCEHARMKVTTPCMSSGSLW-----
                                                                                                                                                                                                                                                                             GIPQHVQRW.
                                                                                                                                                                                                                                                                                            -LRHHHRRWRFTESHEVVDPDQEYEVTVHHLPK------
                                                                                                                                                                                                          EFENVILGDLEQUQIKPDVFTHTSNYFDLMLDY-----CVRLIKESKAYVDDTPPEQM
                                                                                                                                                                                                                         E-----AHOLRYSTTLWNESTHYOILLTSPPHMENHSCF----EHMHHIPAPRPE--
                                                                                                                                                        ATVSCPEMP 307
                                                                                                                                                                         KLEREORVESANRSNSVEKNLSLWEEMVKGSEKGONTACAAKIDM-----SSPNGCMRDP
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                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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946
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WTACA -> KYCYN (IN REF
345

K -> R (IN REF 3).

692

T -> S (IN REF 3).

753

T -> S (IN REF 3).

802

T -> S (IN REF 3).

807

P -> T (IN REF 3).

887

G -> V (IN REF 3).

1461

MISSING (IN REF 3).

1587

G -> V (IN REF 3).

1587

G -> V (IN REF 3).

1697

MW; 6FE8C58045E48A8C CI
                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                          5.0%;
19.2%;
                                                                                                                                                                                                                                                                                                                                                ---SNNDVL----RALARAAPDYKLYGETAIERTOIDHW 83
                                                                                                                                                                                            -SNVTLTLRNLKG-----CCRHQVQIQPFFSSCLNDCLRHS 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WHEP-TRS
WHEP-TRS
WHEP-TRS
WHEP-TRS
                                                                                                                                                                                                                                                                                                                                                                                  48;
                                                                                                                                                                                                                                                                                                                                                                                 Score 87.5; DB pred. No. 14; 48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSPLP -> DKSIA (IN REF. 3).
VC -> AF (IN REF. 3).
NTACA -> KYCYR (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "KMSKS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROLYL-TRNA SYNTHETASE. "HIGH" REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-GLY
                                    gamma
                                     subdivision; pasteurellaceae;
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                                                                                                                                                                                                                                                                                                                                                                                      119;
                                                                                                                                                                                                                                                                                                                                                                                                       Length 1714;
                                                                                                                                                                                                                                                                                                                                                                                                                                CRC64;
                                                                                                                                                                                                                                                                                                                                                                                       Indels 131; Gaps
                                                                                                                                                                                                                                                                                                      -PIPDGDPNHQSK 178
                                                                                                                                                                                                                                                                       -DPNITVETL
                                                                                                                                                                                                                                                                                          192
                                                                                                                                                                                                                                                                          212
                                                                                                                                                                                                                                                         252
                                                                                                                                                                                                                         305
                                                                                                                                                                                                                                          258
                                                                                                                                                                                                                                                                                                                                                                                            17;
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STRAIN=RD / KW20 / ATCC 51907; MEDLINE=95350630; PubMed=7542800;

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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it modified and this content is in no we modified and this creatment is in no we
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Science 269:496-512(1995).

Science 269:496-512(1995).

I CATALTIC ACTIVITY: D-XYLOSE = D-XYLULOSE.

I CATALTIC ACTIVITY: BELONGSIUM IS NECESSARY FOR THE ACTIVITY (BY SIMILARITY).

I SUBCULT: HOMOTETRAMER (BY SIMILARITY).

I SUBCELLULAR LOCATION: CYTOPLASMIC.

I SIMILARITY: BELONGS TO THE XYLOSE ISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 LQIQLHFAHT----QQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLNTNERLCVRFEEL 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Meriick J.M.
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Weldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Myuyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
"MALL" "MALL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
                                                                                                                                                                                                                                                                                                QVETGVKLLWGTANCFTNPRYMSGAATNPNPEVFAWAATQVFNAMNATQRLGGENYVLWG
                                                                                                                                                                                                                                                                                                                                                                                                                 SKLRHHHRRWRETFSHFVVDPD----OEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRLAVCYWHTFCWNGNDMFGLGSLERSWQKNSNL--LAGAE------QKADIAFEFL
                                                                                                                                                                                                                                                                                                                                  ---TTPCMSSGSLWDDNITVETLEAHQL-----RVSFTLWN 225
                                                                                                                                                                                                                                                                                                                                                                              ·IVDILERK 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          collaboration
Foutstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                     EMBL; X13255; CAA31631.1; --
EMBL; X13256; CAA31632.1; --
EMBL; Y00096; CAA688285.1; --
PIR; S03020; S03020;
PIR; S05283; S06283.
                 CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
VARIANT
                                                                                                                 CHAIN
ACT_SITE
ACT_SITE
BINDING
                                                                                                                                                               Prim; pro1082; Labonoxgnase.

PRINTS; PRO0767; DBMONOXGNASE.

PROSITE; PS00084; CU2_MONOXYGENASE_1; 1.

PROSITE; PS00085; CU2_MONOOXYGENASE_2; 1.

PROSITE; PS00085; CU2_MONOOXYGENASE_2; 1.

PROSITE; PS00085; CU2_MONOOXYGENASE_2; 1.

PROSITE; PS00085; CU2_MONOOXYGENASE; CO
                                                                                                                                                                                                                                                                                  InterPro; IPR000323; ...
InterPro; IPR000945; ...
Pfam; PF01082; Cu2_monooxygen; 1.
PRINTS; PR00767; DBMONOXGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict modified and this statement is not removed. Usage by and for send an email to licensee@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- COPACTOR: POO, COPPER, AND ASCORBATE.
-1- PATHWAY: CATECHOLANTHE BIOSYNTHESIS.
-1- SUBGELLULAR LOCATION: EXISTS BOTH IN A SOLUBLE FORM (IN CHROMAFFIN ANCHORED BY AN UNCLEAVED SIGNAL PEPTIDE).
-1- INDUCTION: ACTIVITY IS ENHANCED BY NERVE GROWTH FACTOR (IN SUPERIOR CERVICAL GANCLIA & ADRENAL MEDULLA). TRANS-SYNAPTIC STIMULATION WITH RESERPINE, ACETYLCHED BY ADDILLA. THERE EXIST TWO FORMS OF DBH: DBH-A AND DBH-B, MCNONOXYGPNACE ENMITTY
                                                                                                                                                                                                                                                                                                                                                                            MIM; 223360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <del>1</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND PARTIAL SMEDLINE=88166633; PubMed=3443096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kobayashi K., Kurosawa Y., Fukita K., Nagatsu T., "Human dopamine beta-hydroxylase gene: two mRNA types different 3'-terminal regions are produced through alt polyadenylation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-89160241; PubMed-2922261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOPAMINE BETA-MONOOXYGENASE PRECURSOR (EC 1.14.17.1) (DOPAMINE BETA-
               26
216
398
398
398
170
170
130
330
      ); Glycoprotein; Membrane; S
5 25
6 603 DOPAMINE BET
6 216 POTENTIAL.
8 398 COPPER (POTE
8 398 COPPER (POTE
0 50 N-LINKED (GLA
0 330 N-LINKED (GLA
0 330 N-LINKED (GLA
0 304 A -> S (IN DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Res. 17:1089-1102(1989).
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  COPPER (POTENTIAL)

N-LINKED (GLCNAC

N-LINKED (GLCNAC
(IN
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he soluble and the membrane-bound
                                                                                                                                                    BETA-MONOOXYGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.isb-sib.ch/announce/
                          ) (POTENTIAL).
) (POTENTIAL).
) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IN CHROMAFFIN
                                                                                                                                                                                                          Copper;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       collaboration
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On
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RESULT 7
DOPO_HUMAN
ID DOPO_HUMAN
AC P09172;
DT 01-MAR-1989 (
DT 01-OCT-2000 (

STANDARD;

PRT;

603

(Rel. (Rel. (Rel.

10, 10,

, Created) , Last sequence up, , Last annotation

update)

Ър

δÃ В Qγ В

189

91

NKLGVPY----YCFHDVDIAPEGNSVREYVQNFHH-----

133

δÃ

Score 86; DB: Pred. No. 3.6; 34; Mismatches

71;

Indels

Дb Ş

226 ESTHYQILLTSFPHNENHS------CFEHMHHIP------APRPEE

GREGYETLLNTDLKREREQIGREMOMVVEHKHKIGFKGTLLIEPKPQE

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SOFT
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RESULT 8

KAIR_SON

ID KAIR_S

Q09988

AC Q09988

PT 01-FEE

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DT 01-FEE

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CO Schizz

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Matches 54
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KAIB_SCHPO
Q09898;
01-FEB-1996
                                                                                                                                                        EMBL; 267757; CAA91776.1; -
HSSP; P05132; 1CTP.
InterPro; IPR000719; -
InterPro; IPR000961; -
InterPro; IPR002290; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
PROBABLE SERINE/THREONINE-PROTEIN KINASE C24B11.11C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166
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SPAC24B11.11C.

Schizosaccharomyces pombe (Fission yeast).

Schizosaccharomycetaes; Schizosaccharomycetes;

Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89
                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                         pfam; pf00069; pkinase; 1.
pfam; pf00433; pkinase_C; 1.
pr0SITE; pS00107; pr0TEIN_KINASE_ATP; 1
pr0SITE; pS00108; pr0TEIN_KINASE_DOM; 1
pr0SITE; pS50011; pr0TEIN_KINASE_DOM; 1
                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
    Hypothetical ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --LEGAELSVLQLNTNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYE-VTVHHLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----KPIPDGDPNHQSKNFLVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQL
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535
603
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            protein; Transic
Phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197
535
67627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.9%;
                                    Transferase; Serine/threonine-protein kinase;
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A -> T (IN REF
R -> C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42;
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Pred. No.
                                                                                                                                                                                                                                                              .'
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-> C (IN REF. 2).
39A7A8975111DB5F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    607
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                                                                                                                                                                                                                        "Gemin4: a novel component of the SMN complex that is found in both "gems and nucleoil.";
gems and nucleoil.";
J. Cell Biol. 148:1177-1186(2000).

-I. FUNCTION: THE SMN COMPLEX PLAYS AND IS REQUIRED FOR PRE-MRNA SNRNP ASSEMBLY IN THE CYTOPLASM, AND IS REQUIRED FOR PRE-MRNA SNRNP ASSEMBLY IN THE CYTOPLASM, AND IS REQUIRED FOR PRE-MRNA SNRNP ASSEMBLY IN THE CYTOPLASM, AND IS REQUIRED FOR PROTEING OF SPLICING IN THE NUCLEUS. GEMIN4 COULD SERVE AS A COFACTOR OF SPLICING IN THE NUCLEUS. GEMIN4 COULD SERVE AS A COFACTOR OF SPLICING IN THE SUBUNIT: FORMS A STABLE HETEROMERIC COMPLEX WITH SURVIVAL OF MOTOR IN CHARLES OF STABLE HETEROMERIC COMPLEX WITH SURVIVAL WITH SUBUNIT: FORMS A STABLE HETEROMERIC COMPLEX MITH SURVIVAL WITH SUBUNING SMN), GEMIN3 AND WITH SEVERAL SNRNP SM CORE PROTEINS, INCLUDING B/B', GEMIN3 AND WITH SEVERAL SNRNP SM CORE PROTEINS, INCLUDING B/B', TALLOW AND THE SEVERAL SNRNP SM CORE PROTEINS, INCLUDING B/B', TALLOW AND THE SEVERAL SNRNP SM CORE PROTEINS, INCLUDING B/B', TALLOW AND THE SEVERAL SNRNP SM CORE PROTEINS, INCLUDING B/B', TALLOW AND THE SEVERAL SNRNP SM CORE PROTEINS, INCLUDING B/B', TALLOW AND THE SEVERAL SNRNP SM CORE PROTEINS, INCLUDING B/B', TALLOW AND THE SEVERAL SNRNP SM CORE PROTEINS, INCLUDING B/B', TALLOW AND THE SEVERAL SNRNP SM CORE PROTEINS, INCLUDING B/B', TALLOW AND THE SEVERAL SNRNP SM CORE PROTEINS.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute are no restrictions on its by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                      Charroux B., Pellizzoni L., Perkinson R.A.,
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SUBCELLULAR LOCATION: CYTOPLAMIC AND NUCLEAR. LOCALIZED IN SUBNUCLEAR STRUCTURES NEXT TO COILED BODIES, CALLED GEMS, WHICH SUBNUCLEAR STRUCTURES NEXT TO COILED BODIES, CALLED GEMS, WHICH SUBNUCLEAR STRUCTURES NEXT TO COILED BODIES, CALLED GEMS, WHICH STRUCTURES AND IN THE NUCLEOLUS.
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
F GEMS 4 (GEMIN4) (P97).
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
M; D92E5263C7341F1D CRC64;
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Pred.
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No. 6.5;
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Matches 66
                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restr
                                                    use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                     MEDLINE-56010237; PubMed=7571434;
Schultz U., Koeck J., Schlicht H.J., Staeheli P.;
"Recombinant duck interferon: a new reagent for studying interferon action against hepatitis B virus.";
Virology 212:641-649(1995).
-i- INDUCTION: BY VIRUSES.
                           EMBL; X84764; CAA59235.1;
HSSP; P01574; IAU1.
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                                                                                                                                                                                                                                                             TISSUE=Embryo;
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                            Anas platyrhynchos (Domestic duck).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       357
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DOMAIN 714 735 LEUCINE-ZIPPER (POTENTIAL).

SEQUENCE 1058 AA; 119989 MW; 5EE1FEZEE3538D6B CRC64;
                                                                                                                                                             SIMILARITY: BELONGS TO THE INTERFERON ALPHA,
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               IPR000471;
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                                                                                                                    SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-97186689; PubMed-9034305;

Korobko I.V., Yamamoto K., Nogi Y., Muramatsu M.;

"Protein interaction cloning in yeast of the mouse third largest polymerase II subunit, mRPB31.";

Polymerase II subunit, mRPB31.";

Gene 185:1-4(1997),

-i- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCR

TO NNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES
        This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; F
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae;
                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
DNA-DIRECTED RNA POLYMERASE II 33 KDA POLYPEPTIDE (EC 2.7.7.6) (RPB3)
(RNA POLYMERASE II SUBUNIT 3) (RPB33) (RPB31).
                                                                                                                                                                                                                                                                                                                                                                       RPB3_MOUSE
P97760;
                                                                                                                                                                                                                                                                                                                                                                                              MOUSE
                                   SUBUNIT: KNA FULLIALIA.

SUBCELLULAR LOCATION: NUCLEAR.

MISCELLANDOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES
FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNJ
PERCURSOR. POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                          171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131
                                  PRECURSOR, POLYMERASE II FOR III FOR 5S AND TRNA GENES.
SIMILARITY: BELONGS TO THE RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; E
Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                          SUBUNIT: RNA POLYMERASE II CONSISTS OF 12 DIFFERENT SUBUNITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
      SWISS-PROT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 TVKNSTC-LDDSWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYL 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PQQHAPCSFPDTLLDTNDTQQAAHTALHLLQHLFDTLSSPSTP-AH--W------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADAARLHRRGPRNLHLSINKYFGCIQHFLQNHTYSPC----AWD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---ARHDLLNQLQHH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGAELSVLQLNTNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDDDQEYEVTVHHLPKPIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSAVPGP-LLGLLLLLLGVLAPGGA-----SLRLLDHRALVCSQPGLNC
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56; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       \begin{array}{c} 161 \\ 191 \end{array}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -DGDPN-HQSKNFLVPDCEHARMKVT-TPCMSSGSLWDPNITVETLEAHQLRV
                                                                                                                                                                                                                                                                                                                                                                                                                                  --HVR-----LEAHACFQRIHRL
    entry
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31
67
60
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copyright.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-S4D197AC899BB82F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29;
                              RPB3/RPC5 RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 83;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                  TRIPHOSPHATE = N PYROPHOSPHATE
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2.4;
                             POLYMERASE
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; Murinae; Mus
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                             SUBUNIT
                                                 POLYMERASE
                                                                                                                                                 TRANSCRIPTION
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                                                                                                                                                                                     RNA
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collaboration

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EMBL, J04183; AAA60382.1;
PIR; A30565; A236524.1;
PIR; A30565; A23656.
PIR; A30210; A30510
PIR; A30210; A30510
PIR; A32685; A32685
PIR; B40150; A32685
PIR; B40150; A02150,
R Carbbank; CCSD:54729;
R MIM; B15330; IRR002000
                                                                                                                                                                                                                                                                                                                                                                                  CC LAMB-I ARE POLILACIOSYLATED; SOME OF THE 18 N-GLYCAMAL.

CC LAMB-I ARE POLILACIOSYLATED; SOME OF THE 18 N-GLYCAMS, AND THE PLASMA

CC LAMB-I ARE POLILACIOSAMINOCLYCAMS.

CC LAMB-I ARE POLILACIONAL.

CL LAMB-I ARE POLILACIONAL.

CC LAMB-I ARE POLILACIONAL.

CC LAMB-I ARE POLILACIONAL.

CC LAMB-I ARE POLILACIONAL.

CC LAMB-I ARE 
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PF01299; Lamp; 1.
PR00336; LYSASSOCTDMP.
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POLYLACTOSAMINOGLYCANS.

CAR1SSON S.R., PubMed*2243102;

"The Polylactosaminoglycans of human lysosomal membrane glycoproteins for the polylactosaminoglycans of human lysosomal membrane glycoproteins for the polylactosaminoglycans of human lysosomal membrane glycoproteins for the peride backbones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFIDE BONDS.
MEDLINE-90062189; PubMed-2584229;
"TISSON S.R.'. Fukuda M.;
"""Soomal memb;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carlsson S.R., Fukuda M.;
"Structure of human lysosomal membrane glycoprotein 1. Assignment of fall Chem. 264:20526-20531(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 28-58.

MEDLINE-89104438; PubMed=2912382;
Hildreth J.E., Margella Limed L., Bainton D.F., Holt V.K., Cha Y.,

"O'VCODTOTEINS.", differential of human lysosomal membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 32-416 FROM N.A., AND PARTIAL SEQUENCE.
VILTALA J., CARLESSON S.R., Stabert P.D., FUKUda M.,
membrane glycoprotein with apparent Mr approximately equal to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organization in two genes.",
,, Biol. Chem. 268:9014-9022(1993).
                                                                       В
Homo sapiens (Human)
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                            DЪ
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                                                                                                                                                                                                                                                                                       296 RHSATVSCPEMPD-TPEPIP 314
                                                                                                                                                                                                                                                              144 TRADIDKKYRCVSGTOVHMNNVTVTL-----HDATTOAYLSNSSFSRGETRCEOD-- 193
                                                                                                                                                                                                                                                                                         252 IPAPRPEEEH------ORSMYTLTLRNLKGCCRHOVOIOPEESS------CLMDCL 295
                                                                                                                                                                                                                                                                                                                                                     204 DPNITVETLEAHOLRVSFTLWNESTHYQILLTSFPH--MENH------SCFEHMHH 251
                                                                                                                                                                                                                                                                                                                        86 DESLVIAFGRGHTLTLNET---RNATRYSVOLMSEVYNLSDTHLFFNASSKEIKTVESITD 143
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CONFLICT
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DOMAIN
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Transmembrane; Glycoprotein; Lysosome; Signal 27
CHAIN 28 416
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416 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44773 MW;
                                                                                                                                                                                                                                                                                                                                                                                                     4.68; Score 81.5; DB 1; Length 416;
ive 20; Mismatches 45; Indels 4
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N-LINKED (GLCMAC.
N-LINKED
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POLYLAGTOS GLCNAC.

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POLYLAGTOS MINOGLYCAN.

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POLYLAGTOS MINOGLYCAN.

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(GLCNAC.

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CYTOPLASMIC (POTENTIAL).
FIRST LOMENAL DOMAIN.
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InterPro, IPROU Pfam, PF01299,

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NON_TER 1
DOMAIN <1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
CARBOHYD
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Res. 5:169-176(1998).

-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL)

-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL)

ONE V-LIKE DOMAIN. BELONGS TO THE BIN/MOG SUBFAMILY.

ONE V-LIKE DOMAIN. BELONGS TO THE BIN/MOG SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                      RPB3_HUMAN STANDARD; PRT; 275 AA P19387; O15161; O1-NOV-1990 (Rel. 16, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation update DNA-DIRECTED RNA POLYMERASE II SUBUNIT 3) (RPB33) (RPB3 POLR2C OR A-152E5.7.
                                                                                                                                                                                           HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                           Eukaryota; Metazoa; C
                                                                                                                                                                                                                                                                                                                                                                                                     177 SKNFLVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTL-WNESTHYQILLT 235
               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                           367
                                                                                                                                                                                                                                                       451
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                                                                                                                                                                                                                                                                                                                                          SFPHMENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCL 295
                                                                                                                                                                                                                                                       RRPAPMGCPEWVQAPAPSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                   32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            large proteins in vitro."; 5:169-176(1998).
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299
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POTENTIAL.

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTE

N-LINKED (GLCNAC. .) (POTE
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 81.5; D
Pred. No. 12;
13; Mismatches
                                                Craniata;
                                  Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane
                                                                                                          update)
POLYPEPTIDE
                                                                                             (RPB31).
                                                  Vertebrata;
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                                     Hominidae;
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                                                  Euteleostomi,
                                                                                                             2.7.7.6)
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MEDIINE-99425270; PubMed=10493829;
Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R.,
Loftus B.J., Kim U.-J., Sneddon V.P., Barnstead M., Cronin L.,
Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,
Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,
Elchler E.E., Harris P.C., Venter J.C., Adams M.D.;
Elchler E.E., Harris P.C., Venter J.C., Adams M.D.;
Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q.";
Genomics 60:295-308(1999).
Genomics 60:295-308(1999).
Genomics 60:295-308(1999).
The FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION ON THE FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION THE FUNCTION THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
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"The amino acid sequence of the human RNA polymerase II 33-kDa subunit hRPB 33 is highly conserved among eukaryotes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Skeletal muscle;
Bruno T., di Padova M., de
Passananti C., Fanciulli M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98201707; PubMed=9540830; Dammann R., Pfeifer G.P.;
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                                                                                                                                 Nuclear protein.
DOMAIN 88
CONFLICT 194
SEQUENCE 275 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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EMBL;
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POLR2J AND POLR2C SUBUNITS INTERACT WITH EACH OTHER.
POLR2J AND POLR2C SUBUNITS INTERACT WITH EACH OTHER.
SUBCELLULAR LOCATION: NUCLEAR.
MISCELLANDOUS: THEREE DISTINCT ZINC-CONTAINING RNA POLYMERASES AF FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA PRECURSOR, POLYMERASE II FOR THE WRNA PRECURSOR, AND POLYMERASE III FOR SS AND TRRA GENES.
SIMILARITY: BELONGS TO THE RPB3/RPC5 RNA POLYMERASE SUBUNIT FAMILY.
54 NSTCLDDSWI-HPRNLTPSSPKDLQIQLHFAHTQQGDLF-PVAHIEWTLQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: N. NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE
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                                                                                                                                                                                                                                                                  A36264; A36264.
180663; -.
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                                                           Similarity
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nilarity 20.3%;
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194
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141 RWRFTFS	175	18	
141 RWRFTFS-HFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNELVP 183	175 KWNPTAGVAFEYDPDNALRHTVYPKPEEWPKSEYSELDEDESQAPYDPNGKPERFYYNVE 234	184 DCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVS 220	235 SCGSLRPETIVLSALSGLKKKLS 257

Search completed: July 17, 2001, 11:21:05 Job time: 159 sec

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OM protein -
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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pIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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1764
1 MGAARSPPSAVPGPLLGLLL......VSCPEMPDTPEPIPDYMPLW 320
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                               219241 seqs, 76174552 residues
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

11 22 33 44 44 47 65 66 67 77 10 11 11 11 11 11 11 11 11 11	ult No.
92 88.5 88.5 88.5 87.8 87.8 87.5 88	Score
44444444444444444444444444444444444444	Query Match Le
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pyochelin syntheta	hypothetical prote prochelin syntheta	DNA polymerase III sensor protein evg	RNA-directed KNA F sugar hydrolase [i	pol polyprotein -	hypothetical prote	hypothetical prote	hypothetical Figure 1ysosome-associate	ig heavy chain C r	hypothetical prote protein F12K11.6 {

ALIGNMENTS

RESULT 2 I51544 IS beta-chain - African clawed frog MHC class II beta-chain - African clawed frog) C; Species: Xenopus laevis (African clawed frog) C; Species: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jan-2000 C; Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jan-2000	Query Match Best Local Similarity 22.6%; pred. No. 6.8; Best Local Similarity 22.6%; pred. No. 6.8; Matches 67; Conservative 33; Mismatches 101; Indels 96; Gaps 15; Matches 67; Conservative 33; Mismatches 101; Indels 96; Gaps 15; Matches 67; Conservative 33; Mismatches 101; Indels 96; Gaps 15; Matches 67; Conservative 33; Mismatches 101; Indels 96; Gaps 15; Matches 67; Conservative 32; Mismatches 101; Indels 96; Gaps 15; Matches 67; Conservative 33; Mismatches 101; Indels 96; Gaps 15; Matches 67; Conservative 33; Mismatches 101; Indels 96; Gaps 15; Matches 67; Conservative 33; Mismatches 101; Indels 96; Gaps 15; Matches 67; Conservative 33; Mismatches 101; Indels 96; Gaps 15; Matches 67; Conservative 426; Indels 96; Inde	RESULT 1 H84779 hypothetical protein At2g36370 [imported] - Arabidopsis thaliana (C.Specles: Arabidopsis thaliana (mouse-ear cress) (C.Specles: Arabidopsis thaliana (mouse-ear cress) (C.Specles: Arabidopsis thaliana (mouse-ear cress) (C.Specles: O2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 (C.Y.C.Specles: O2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 (C.Y.Speckers: O2-Feb-2001 #sequence of C.Y.Speckers: O2-Feb-2001 #sext_change 02-Feb-2001 (C.Y.Speckers: O2-Feb-2001 #sext_change 02-Feb-2001 (C.Y.Speckers: O2-Feb-2001 #sext_change 02-Feb-2001 (C.Y.Speckers: O2-Feb-2001 #sext_change 02-Feb-2001 (C.Y.Speckers: O2-Feb-2001 #sext_change 02-Feb-2001 *c.Y.Speckers: O2-Feb-2001 #sext_change 02-Feb-2001 *c.Y.Speckers: O2-Feb-2001 #sext_change 02-Feb-2001 *c.Y.Speckers: O2-Feb-2001 #sext_change 02-Feb-2001 *c.Y.Speckers: O2-Feb-2001 *c.

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glycoprotein VP7 precursor - human rotavirus B
C;Species: human rotavirus B
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_cha
C;Accession: A37080
R;Chen, G.M.; Hung, T.; Mackow, E.R.
Virology 178, 311-315, 1990
A;Title: Identification of the gene encoding the group B rot.
A;Reference number: A37080, MUID:90357782
A;Accession: A37080
A;Molecule type: genomic RNA
A;Cross-references: EMBL:M33872; NID:g210569; PIDN:AAAA2675
A;Monecule type: genomic RNA
A;Cross-references: EMBL:M33872; NID:g210569; PIDN:AAAA2675
                                                                                                                                                                                                                           A;Map position: segment 9
C;Superfamily: rotavirus B glycoprotein vp7
C;Reywords: capsid protein; glycoprotein
F;11.5/Domain: signal sequence #status predicted <SIG>
F;16-249/Product: glycoprotein vp7 #status predicted <Vp7>
F;45,91,105/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                         A; Cross references: EMBL:M33872; NID:g210569; A; Note: the authors translated the codon GAT f
                                                                                                                                                                                         Query Match
Best Local Similarity
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R;Sato, K.; Flajnik, M.F.; Pasquier, L.D.; Katagiri, M.; Kasahara, M.
J. Immunol. 150, 2831-2843, 1992
A;Title: Evolution of the MHC: isolation of class II beta-chain cDNA /
A;Reference number: I51539; MUID:93203604
A;Raccession: I51544
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-260 <SAT>
A;Residues: 1-260 <SAT>
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                                  104 ASILYLEGAELSVLQLN----TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEV 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NFLVPDCEHARMKVTTPCMSSGSLWDPNITVETL----EAHQLRVSFTLWNESTHYQI-
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64; Conservative
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22.78;
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Pred. No. 3.3;
34; Mismatches
                                                                                                                                                                                                                                                                                                                                                       PIDN:AAA42675
for residue 88
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                                                                                                                                                            82;
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                                                      A:Gene: FlyBase:Dvir/salm
A:Cross references: FlyBase:FBgn0013137
C:Keywords: DNA binding; transcription;
                                                                                                 A; Didicule type: mRNĀ
A; Molecule type: mRNĀ
A; Residues: 1-1402 <SCH>
A:Cross-references: EMBL; Z27444; NID: g426461; PID: g426462
                                                                                                                                                                                                A;Reference number:
A;Accession: S42748
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                                                                                                                                                                                    A; Status:
                                                                                                                                                                                                                                                                          finger protein - fruit fly (Drosophila virilis) (fragment) c;Specias: Drosophila virilis C;Date: 20-oct-1994 *Sequence_revision 26-May-1995 *text C;Accession: S42748
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C;Species: Nicotiana glutinosa
C;Species: Nicotiana glutinosa
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 05-Nov-1999
C;Accession: A54810
R;Whitham, S; Dinesh-Kumar, S.P.; Choi, D.; Hehl, R.; Corr, C.; Baker, B.
Cell 78, 1101-1115, 1994
A;Title: The product of the tobacco mosaic virus resistance gene N: similarity to tol
A;Accession: A54810
A;Accession: A54810
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A;Introns: 160/2; 525/3; 616/3 1139/3
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A:Molecule type: DNA
A:Residues: 1-1144 <WHI>
A:Cross-references: GB:U15605; NID:g558886; PIDN:AAA50763.1; PID:g558887
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Best Local S
Matches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
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                                                                                                                                                                                                                                                                                                                                                                                                      674
                                                                                                                                                                                                                                                                                                                                                                                                                                          620 SLRRIDLSWSKRLTRTPDFTGMPNLEYVNLYQCSNLEEVHHSLGCCSKVIGLY----L
                                                                                                                                                                                                                                                                                                                                                                                                                                       292 NDC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  254 APRPEEFHORSNVTLT----LRNLK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         560 MGRSSTHYAIDYLPNNLRCFVCTNYPWESFPSTFELKMLVHLQLRHNSLRHLWTETKHLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 LWNESTHYQI-----HAIP 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      504 DPGERSRLWLAKEVEEV-MSNNTGTMAMEAIWVSSYSSTLRESNOAVKNMK--RLRV-FN 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 DPNHOSKNELVEDCEHARMKVTTPCMSSGSLW------DENITVETLEAHOLRYSFT 222
                                                                                                                                                                                                                                                                                                                                                       u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 FCPLSDSLIGMYCDTQLSDTYFEISTGGTYEVTDIPE 170
                                                                                                                                                                                                                                                                                                                                                                                    NDCKSLKRFPCVNVESLEYLGLRSCDSLEKLPE 706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCNILAIDVENASMDENVELQSTNNCSKYNA-NKVHHVKLPRGEEWESYS-----KNLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 20.7
44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----VSFTLWNESTHYQILLTSFPHMENHSCFEHMHHIPAPRPEEFHORSNVTLTLRNLK 274
                                                                                                                                                                                                                                                             #sequence_revision 26-May-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                   ---LRHSATVSCPEMPDTPE 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.0%; bu.
, 20.7%; Pre
              5.0%;
                                                                                                                                                                                                                        Library, November
          Score
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29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 88.5;
Pred. No. 30;
                                                       regulation
          88
       DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------GCCRHQVQIQPFFSSCL 291
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   Length
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1402;
                                                                                                                                                                                                                                                          24-Sep-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83;
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RESULT VGXRHB

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Matches

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us-09-488-728-4_copy_1_320.rpr

DE GALSYLOLTERENCY PRESENT CONTROL OF THE PLANT CONTROL OF THE PROPERTY ASSESSMENT FOR SOLUTION OF THE PROPERTY OF THE PROPERY	al Similarity 21.1%; Pred. Mismatches 114; Indels 129; Gaps 74; Conservative 3; Mismatches 114; Indels 129; Gaps 74; Conservative 3; Mismatches 114; Indels 129; Gaps 174; Conservative 3; Mismatches 114; Indels 129; Gaps 174; Conservative 3; Mismatches 114; Indels 129; Gaps 174; Conservative 3; Gaps 174; Conservative 3; Gaps 174; Gaps	Best Local Similarity 21.1%; Pred. No. 30; Matches 74; Conservative 33; Mismatches 114; Indels 129; Ga Matches 74; Conservative 33; Mismatches 1 MGAARSPPSAVPGPLIGLLILLGVLAPGGASLRILDHRALVCSOPGLNCTVKN 1 MGAARSPPSAVPGPLIGL
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A; ACCESSION. A310.

A; Molecule type: mRNA
A; Residues: 713-964 < LIN>
A; Molecule type: mRNA
A; Residues: 713-964 < LIN>
A; Molecule type: mRNA
A; Residues: 713-964 < LIN>
A; Molecule type: mRNA
A; Residues: 713-964 < LIN>
A; Molecule type: mRNA
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A; Molecule type: mRNA
A; Molecule type
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A;Experimental source: carcinoma cell line A431-7
A;Experimental source: carcinoma cell line A431-7
R;Xu, Y.; Ishli, S.; Clark, A.J.L.; Sullivan, M.; Wilson, R.K.; Ma, D.P.; Roe, B.A.;
R;Xu, Y.; Ishli, S.; Clark, A.J.L.; Sullivan, M.; Wilson, R.K.; Ma, D.P.; Roe, B.A.;
Rature 309, 806-810, 1984
A;Title: Human epidermal growth factor receptor cDNA is homologous to a variety of RN
A;Reference number: A00642; MUID:84245835
A;Accession: A00642; MUID:84245835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecule type: mRNA.

Molecules: 1-1210 <ULL>
Residues: 1-1210 <ULL>
Cross-references: EMBL:X00588; NID:g31113; PIDN:CAA25240.1; PID:g757924

Cross-references: EMBL:X00588; NED:g31113; PIDN:CAA25240.1; PID:g757924

Cross-references: EMBL:X00588; NID:g31113; PIDN:CAA25240.1; PASS

Note: the authors translated the codon AAG for residue 540 as ASN

Ishii, S.; Xu, Y.; Stratton, R.H.; Roe, B.A.; Merlino, G.T.; Pastan, I.

Ishii, S.; Xu, Y.; Stratton, R.H.; Roe, B.A.; Merlino, G.T.; Pastan, I.

Oc. Natl. Acad. Sci. U.S.A. 82, 4920-4924, 1985

Title: Characterization and sequence of the promoter region of the human epidermal ritle: Characterization and sequence of the promoter region of the human epidermal Reference number: A25772; MUID:85270438

Reference number: A25772; MUID:85270438
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reference number: S30024; MUID:88217333

Reference number: S30024; MUID:88217333
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Biol. Chem. 266, 1746-1753, 1991
Fills: Contributory effects of de Novo transcription and premature transcript termi
Reference number: A38672; MUID:91107677
;Accession: A38672
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Residues: 1-29 <HA2>
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ERIWDGKDLDGVPEEPDEDVEPFERIDDKTIQHFSHEHYLRLNIRNGVFDADSFCQACII 401
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F;1047-1210/Region: inhibitory
F;128 175,352,413,444,528,603/Binding site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A/Cross-references: GDB:120610; OMIM:131550
A/Map position: 7p12.3-7p12.1
C/Superfamily: epidermal growth factor receptor; protein kinase homology
C/Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phosphopro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Functional independence of the epidermal growth factor receptor from a domain A;Reference number: A33331; MUID:90003233 Schontents: annotation; internalization signal C;Comment: Binding of EGF to the receptor leads to internalization of the EGF-receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-1210/Product: EGF receptor #status predicted <MAT>
25-645/Domain: extracellular #status predicted <EXT>
25-00/Domain: EGF receptor extracellular domain repeat 

390-600/Domain: EGF receptor extracellular domain repeat 

646-668/Domain: transmembrane #status predicted <TMMS</td>

710-975/Domain: intracellular #status predicted <TMMS</td>

718-726/Region: protein kinase homology <KIN>

999-1046/Region: coated-pit mediated internalization sign

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A; Contents: annotation; receptor activity
A; Note: the EGF receptor (and other tyrosine kinases) can nick double-stranded DN Cell 59, 33-43; Lazar, C.S.; Lund, K.A.; Welsh, J.B.; Chang, C.P.; Walton, G.M.; De A. Title: S. 33-43; 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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A;Residues: 25-30,'S',32-51;454-467 <WEB>
R;Russo, M.W.; Lukas, T.J.; Cohen, S.; Staros, J.V.
J. Biol. Chem. 260, 5205-5208, 1985
A;Title: Identification of residues in the nucleotide binding site of the epidermal grow A;Accession: A60143; MUID:85182650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Mroczkowski, B.; Mosig, G.; Cohen, S.
Nature 309, 270-273, 1984
1015 EYLIPQQGFFSSPSTSRTPLLSSLSATSNNSTVACIDRNGLQSCPIKEDSFLQRYSSDPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: ATP-stimulated
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A; Residues: 740-744, 'X', 746-747 < RUS>
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A;Accession: A23062
A;Molecule type: mRNA
A;Residues: 1028-1210 <SIM>
                                                                  179 NFLVPDCEHARNKVT--TPCMSSGSLWDPNITVETLEAHQLRV-----SF-----
                                                                                                                                                                                                                                                                                897 VWSYGVTVWELMTFGSKPYDGIPASEISSI-LEKGERLPQPPICTIDVYMIMVKCWMIDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                    DSRPKFRELITEFSKMARDP-QRYLVIQGDERMHLPSPTDSNFYRALMDEEDMDDVVDAD 1014
                                                                                                                                                                                              KLRHHHRRWRETTFSHEVVDPDQEYEVTV----HHLPKPI-----PDGDPNHQSK
                                                                                                                                                                                                                                                                                                                                                  LFPVAHIEWTLQTDASILY--LEGAELSVLQLNTNERL-----CVRFEFL------S 133
                                                                                                                                                                                                                                                                                                                                                                                                                         DLAARNYLVKTPQHVKITDFGLAKLLGAEEKEYHAEGGKVPIKWMALESILHRIYTHQSD 896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLGICLTSTVQLITQIMPFGCLLDYVREHKDNIGSQYLLNWCVQIAKGMNYLEDRRLVHR 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---PRNLTPSSPKDLQIQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 22.6
93; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   can nick double-stranded DNA hang, C.P.; Walton, G.M.; Der, C.J
                                                                                                                                                                                                                                                                                        955
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В Qy B Qy Вb ρy В QΥ В δÃ

enzyme;

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A;Gene: FlyBase:Aats-glupro
A;Cross-references: FlyBase:FBgn0005674
C;Superfamily: Drosophila multifunctional amino acid--tRNA ligase; &
C;Keywords: aminoacyl-tRNA synthetase; ATP; ligase; multifunctional
                                                                                                                                            N;Alternate names: multifunctional amino acid--tRNA ligase (EC 6.1.1.-) - fruit fly (Drosophila melanoga C;Species: Drosophila melanogaster C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 R;Cerini, C.; Kerjan, P.; Astier, M.; Gratecos, D.; Mirande, M.; Semeriva, M. A;Title: A component of the multisynthetase complex is a multifunctional aminoacyl-transcension: S18644
A;Accession: S18644
MUID:92097547
                                                                                           C; Genetics:
                                                                                                A;Cross-references: GB:M74104;
                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-1714 <C
                                                                                                                                                                                                                                                                                                                             RESULT
S18644
                                                                                                                                                                                                                                                                                                                                                                                          ДЬ
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A;Introns: 166/3; 179/3; 208/1
A;Note: F1P2.40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local s
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submitted to the Protein St
A;Reference number; Z23010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F1P2.40 - Arabidopsis thaliana C. Species: Arabidopsis thaliana (mouse-ear cress) C. Date: 04-Feb-2000 #Sequence_revision 04-Feb-2000 #text_change C. Accession: T45709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: T45709
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T45709
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                                                                                                                                                                                                                                                                                                                                                                                        163
                                                                                                                                                                                                                                                                                                                                                                                                           285 PFF---SSCLNDC
                                                                                                                                                                                                                                                                                                                                                                                                                     103 DPNPEPRSFPYSVKQQCWEKAEKIKGRDPERWRRDHLGNIVFRKLVGCPGCLCHDYDHIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                  235 -----TSFPHMENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGC----CRHQVQIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 NERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNFL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53 ----SSSSPSKTRPELSSGS---PNRNTGEARGGKVKTSATLLDRE---EMGLFPGSGYG 102
                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHOLRVSFTLWNESTHYQILL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SRRICNLLIFFVKLNH------KNLSIDSDNPQ----HSAMKP----DPTRRRNRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GALTEDSIDDTFLPVPEYINQSVPKRPAGSVQNPVYHNQPLNPAPSRDPHYQDPHSTAV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNLKGCCRHOVOIOPFFSSCLN----DCLRHSATVSCPEMP-DTPEPIPDYMP 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 22.8%;
44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -TLWNESTHYQILLT-----SFPHMENHSCFEHMHH----IPAPRPEEFHQRSNVTLTL 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -GNPEYLNTVQP----TCVNSTFDSPAHWAQKGSHQISLDNPDYQQDFFP 1178
                                                                                                                    <CER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.0%;
                                                                                 NID:g157563; PIDN:AAA28594.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brottier,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 87.5; Di
Pred. No. 5.1;
20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database, November 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P.; Wincker, P.; Cattolico, L.; Artiguenave, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82;
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                                                                               PID:g157564
                     amino
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me; protein
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us-09-488-728-4_copy_1_320.rpr

GIPQHYORMYDLITAOPLIOKVIQSIPEDAKVERSPOSSEEQTPAKTGERAVERS GIPQHYORMYDLITAOPLIOKVIQSIPEDAKVERSPOSSEEQTPAKTGERAVEDAKTORM	4.480/Domain: glutami 35-800/Domain: amino a 37-872/Domain: amino a 31-946/Domain: amino a 31-946/Domain: amino a 30-1025/Domain: amino a 30-1025/Domain: amino 355-1100/Domain: amino 129-1173/Domain: amino 139-1173/Domain: amino 139-1173/Domain: amino 139-1173/Domain: amino 139-1173/Domain: amino 139-1173/Domain: amino 129-1173/Domain: amino
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4
N;Alternate names: GFRalpha-3
C:Species: Mus musculus (house mouse)
C;Date: 21-May-1998 #sequence_revision 29-May-1998 #text_change 02-Jun-2000
                                                            GPI-linked receptor precursor - mouse N; Alternate names: GFRalpha-3 C; Species: Mus musculus (house mouse)
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A; Residues: 1-196, 'T', 198-534, 'C', 536-603 < LAM>
A; Residues: 1-196, 'T', 198-534, 'C', 536-603 < LAM>
A; Cross-references: EMBL:Y00096; NID:g30455; PIDN:CAA68285.1; PID:g30456
A; Note: part of this sequence was confirmed by protein sequencing
A; Note: 502-Leu and 507-G1y were also found
R; Li, B: Tsing, S: Kosaka, A.H.; Nguyen, B.; Osen, E.G.; Bach, C.; Chan, H.; Barnett,
A; Title: Expression of human dopamine beta-hydroxylase in Drosophila Schneider 2 cells.
A; Reference number: S61362; MUID:96132606
A; Residues: 16-34 < LIB>
C: Keywords: Catecholamine biosynthesis; copper; glycoprotein; monooxygenase; oxidoreduct; 125/Domain: signal sequence #status predicted < SIC>
E: 26-603/Product: dopamine bots ynthesis; predicted < SIC>
Expression: Signal sequence #status predicted < SIC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: peptidylglycine monooxygenase I homology (Keywords: catecholamine biosynthesis; copper; glycoprotein; monooxygenase; oxidoreduct F;1-25/Domain: signal sequence #status predicted <SIGTProduct: dopamine beta-hydroxylase #status predicted <MAT> F;282-505/Domain: peptidylglycine monooxygenase I homology <PGM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBO J. 6, 3931-3937, 1987
A;Title: The primary structure of human dc
A;Reference number: S06283; MUID:88166633
A;Accession: S06283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross references: EMBL:X13255; NID:g30473; PIDN:CAA31631.1; PID:g30474
A;Note: 304-Ser and 535-Cys were also found; the amino acid exchange at residue R;Lamouroux, A; Vigny, A,; Biguet, N.F.; Darmon, M.C.; Franck, R.; Henry, J.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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                                                                                                                                                                                                                  226
                                                                                                                                                                                                                        275 GCCRHQ-VQIQPFFSSCLNDCLRHSATVSC-PEMPDTP 310
                                                                                                                                                                                                                                                175 QMGL-----QRVQLLKPNIPEPELPSDAC---TMEVQAPNIQIPSQETTYWCYIKELPK
                                                                                                                                                                                                                                                                                                                       127 EGLTLLFKRPFGTCDD----KDYLIED-----GTVHLVYGILEEPFRSLEAINGSGL 174
                                                                                                                                                           13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 LTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTL------QTDASILY----- 108
                                                                                                                                                                                      GFSRHHIIKYEPIVTKGNEALVHHMEVFQCAPEMDSVP 263
                                                                                                                                                                                                                                                                                 RVSFTLWNESTHYQILLTSFPHME--NHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNL-K 274
                                                                                                                                                                                                                                                                                                                                                                                            GELENADLYVLWTD------GDTAYFADAWSDQKGQIHLDPQQDYQLLQVQRTP 126
                                                                                                                                                                                                                                                                                                                                                            ----KPIPDGDPNHQSKNFLVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQL
                                                                                                                                                                                                                                                                                                                                                                                                                               --LEGAELSVLQLNTNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDFDQEYE-VTVHHLP 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LQGSAPRESPLPYHIPLDPEGSL----ELSWNVSYTQEAIHFQLLVRRLKAGVLFGMSDR 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.98;
19.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 86;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
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                                                                                                                                                                                                                                                    225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14;
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was
A;Map position: 1L
C;Superfamily: unassigned
                                  A;Cross-references: EMBL:267757; PIDN:CAA91776.1; GSPDB:GN00066; SPDB:SPAC24B11.11c
                                                                                                                    A; Molecule type: DNA
A; Residues: 1-607 < ODE>
A; Cross references: EMBL:267757; NID:91061288; PIDN:CAA91776.1; PID:91061299
A; Cross references: EMBL:267757; NID:91061288; PIDN:CAA91776.1; PID:91061299
Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
A; Reference number: Z21786
A; Accession: T38338
                                                                                              A; Molecule type: DNA
A; Residues: 1-607 < OI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;92,145,306/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: DDBJ:AB008833; NID:92627159; PIDN:BAA23562.1; PID:92627160 C;Summent: This protein plays a distinct role in cell survival and differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: JE0082
A;Molecule type: mRNA
A;Residues: 1-397 <NOM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Nomoto, S.; Ito, S.; Yang, L.X.; Kluchi, K. Blochem. Biophys. Res. Commun. 244, 849-853, 1998 A; Title: Molecular cloning and expression analysis A; Reference number: JE0082; MUID:98205811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession: JE0082
R; Nomoto, S.; Ito, S
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                   241 VTPNCLDLRSFCR----ADPLCRSRLMDFQTH 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                               266 VTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRH 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194 LA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             209 VETLEAHQLRVSFTLWNESTHYQILLTSFPHMENHSCFEHMHHIPAPR---PEEFHQRSN 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 LNTNERLCVRFEFLSKLRHHHRRWRFTFS----HFVVDP-----DQE-----YEVTVHHL 164
                                                                                                             preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                 preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 DDSWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MGAARSPPSAVPGPLLGLLLLLGVLAPGGASLRLLDHRALV--CSQPGLNCTVKNSTCL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PWKM-----NLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYGEAG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PKPIPDGDPNHQSKNFLVPD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LRNSSLIDCRC------HRRMKHQATCLDIYWTVHPARSLGDYELDVSPYEDTVTSK 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KAAYQHLGSCTSSLSRPLPLE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGLSWSPRP----PLLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEA-NPAC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82;
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Ser/Thr or
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Pred. No. 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 397;
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Tyr-specific

protein

kinases;

protein

kinase hom

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C;Keywords: ATP F;206-508/Domain: protein kinase homology <KIN> F;214-222/Region: protein kinase ATP-binding motif
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A;Residues: 1-1151 <OLI>
A;Cross-references: EMBL:299126; PIDN:CAB16191.1; GSPDB:GN00066; SPDB:SPAC26H5.05
A;Experimental source: strain 972h-; cosmid c26H5
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Matches 60; Conserv
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Search completed: July 17, 2001, 11:19:58 Job time: 152 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 4.8%; Score 84.5; I Best Local Similarity 25.1%; Pred. No. 64; Matches 43; Conservative 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           139 HRRWRFTFSHFVVDDDQEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARMKVTTPCMS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           258 DILTTANSEWLVRLLYAFODTSNIYLAMEFYPGGDFRTLLSNS------GYLRDH 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89 DLFPVAHIEWTLO-----TDASILYL-----EGAELSVLQLNTNERLCVRFEFLSKLRHH 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              258 EEFHQRSNV-----TLTLRNLKGCCRHQVQIQPFFS 288
                                                                                                                                                                                                                                                                                                                                                                                                                           232 FSVNHLPAINEHKWKSRVETNMLF-----ELRIKSNDNQSVPFEYLRLPSWAHREDKK 284
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                                                                                                                                                                                                                                                                                                      285
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                                                                                                                                                                                                                                                                                                  RSSKPOPLOPDPE---TVIHLVPTVLAGD----KSSVVKTCCTRCLLRERKRNARSQAT 336
                                                                                                                                                                                                                                                                                                                                  TESH-EVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNELVPDC-----EHARMKVT 193
                                                                                                                                                                   Conservative
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Maximum DB :
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perfect score:
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Maximum Match 100%
Listing first 45 summaries
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1: /cgn2_6/ptodata/2/
2: /cgn2_6/ptodata/2/
3: /cgn2_6/ptodata/2/
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Match
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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3 US-09-022-255-10
3 US-09-022-656-10
3 US-09-022-253-10
3 US-09-022-259-10
4 US-09-022-259-10
4 US-09-022-259-2
5 US-09-022-255-2
3 US-09-022-255-2
3 US-09-022-256-2
3 US-09-022-259-2
3 US-
US-08-475-035-4

US-08-484-438-7

US-08-073-807A-16

US-08-073-807A-17

US-08-073-807A-18
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RESULT 1
US-08-620-694A-10
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                                                                                                                                                                                      MEDIUM TYPE: FLOPPY ULSA
COMPUTER: Apple Power Macintosh
COMPUTER: Apple Power Macintosh
COPERATING SYSTEM: Apple Operating System 7.5.5
COPERATING SYSTEM: Apple Operating System 7.5.1
SOFTWARE: MICROSOft Word-for Apple, Version 6.0.1
SOFTWARE: MICROSOft Word-for Apple, Version 10.01
CURRENT APPLICATION DATA:
CLASSIFICATION MOMBER: USSN 08/538,765
APPLICATION MOMBER: USSN 08/538,765
APPLICATION MOMBER: USSN 08/538,765
APPLICATION MOMBER: USSN 08/538,765
APPLICATION MOMBER: USSN 08/410,535
APPLICATION MOMBER: USSN 08/410,535
APPLICATION MOMBER: USSN 08/410,535
APPLICATION MOMBER: 345
CLASSIFICATION: 435
CLASSIFICATION MOMBER: 34.695
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TOPOLOGY: 1:

MOLECULE TYPE:

US-08-620-694A-10
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APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                               TELEFAX: (206)
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: J. STREET: Seattle CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: I
                                                                                                                               REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 26
REFERENCE/DOCKET NUMBER: 7000
TELECOMMUNICATION INFORMATION: (206)587-0430
                                              SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
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51 University Street
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US-08-188-582-20
US-08-646-715-20
US-08-211-942-17
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US-08-749-159A-3

US-09-130-032A-3

US-09-130-032A-3

US-07-964-589-2

PCT-US93-02024-2

US-08-771-602D-2

US-08-771-602D-2

US-09-232-446B-2

US-09-232-446B-2

US-09-284-033-2

US-08-779-834B-2
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US-08-930-996A-9
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Sequence 8, Appli
Sequence 20, Appl
Sequence 20, Appl
Sequence 17, Appl
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e 9, Appli
e 9, Appli
5. 5266464
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Matches 320; Query Match Best Local Similarity

Conservative

Length 866;

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ZIP: 98101

COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION: DATA:
APPLICATION NUMBER: US/09/022,255
CLASSIFICATION:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Spriggs, Melanie
APPLICANT: Panslow, William
TITLE OF INVENTION: NO. 6072033el Receptor That Binds IL-17
RUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 TNERLCVRFEFLSKLRHHHRKWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 TNERLCVRFEELSKLRHHHRRWRFTFSHFVVDDDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SWIHPRNLTESSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 1764; DB 2;
100.0%; Pred. No. 8.9e-177;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                       APPLICANT: Yao, ZHENYALICANT: Spriggs, Melanie
APPLICANT: Spriggs, Melanie
APPLICANT: Spriggs, Melanie
TITILE OF INVENTION: No. 6072037el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-022-696-10
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                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 01
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 60,200
Patent No. 60,200
Pameral INFORMATION:
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              AFFILING DATE: 23 MARCH 199,
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-022-255-10
                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
320; Conservative
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                   FILING DATE
                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 TNERLCVRFEELSKLRHHHRRWRFTFSHFVVDADDQEXEVTVHHLPKPIPDGDANHQSKNF 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0, Application US/09022696
6072037
                                                                                                                                               08/620,694
                                                                                                                                                                                                          US/09/022,696
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                                                                                                                                                                                                                                 Version 6.0.1
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RESULT 2 US-09-022-255-10

Sequence 10,

Patent No. 6072033
GENERAL INFORMATION:

0; Application US/09022255

APPLICANT:

Yao,

Zhengbin

COUNTRY:

WA USA

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> 241 241 181

γQ В Qy В

APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
TELECOMMUNICATION INFORMATION:
TELECHONE: (206)587-0430

PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/620,694
FILING DATE: 21 MARCH 1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:

TELEPAX: (206)
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids

TELEFAX: (2

TELEPHONE:

(206)

10:

TELECOMMUNICATION INFORMATION:

206)587-0430

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MOLECULE TYPE: protein US-09-022-696-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   망
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SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYDE: amino acid
THORTOGO
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US-08-978-773-4
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Sequence 4, Application US/08978773

Patent No. 6083906

Patent No. 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240
181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240
181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 TNERLCVRFEFLSKLRHHHRRWRETFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
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                                                        PILING DATE:
CLASSIFICATION: 530
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/052,525
APPLICATION NUMBER: 27 NOVEMBER 1996
FILING DATE: 27 NOVEMBER 1996
CLASSIFICATION: 530
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
NAME: Perkins, Patricia Anne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple PowerMacintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
OPERATING SYSTEM: Apple Operating Software: Microsoft Word for PowerMacintosh. Version 6.0.1
SOFTWARE: Microsoft Word for PowerMacintosh. Version 6.0.1
APPLICATION NUMBER: US/08/978,773
APPLICATION NUMBER: US/08/978,773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWIHPRNLTPSSPKDLQTQLHEAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENHSCFEHMHHIPAPRPEEFHORSNYTLTLRNLKGCCRHOVOIOPEFSSCLNDCLRHSAT 300
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NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2623
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51 University Street
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US-08-978-773-4
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Best Local Similarity 100.
Matches 320; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acid
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US-09-022-253-10
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TYPE: amino acid
TOPOLOGY: 11
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                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Applicat patent No. 6096305 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 TNERLCVREEFLSKLRHHHRRWRETFSHEVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 TNERLCVRFEELSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 SWIHPRNLTPSSPKDLQIQLHEAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                      APPLICANT: Yao, Zhen
APPLICANT: Spriggs,
APPLICANT: Fanslow,
APPLICANTINEERION:
                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh
COMPUTER: Apple Power Macintosh
COPERATING SYSTEM: Apple Operating System 6.0.

SOFTWARE: Microsoft Word for Apple, Version 6.0.

SOFTWARE: Microsoft Word for Apple, Version 6.0.

APPLICATION NUMBER: US/09/022,253

APPLICATION NUMBER: US/09/022,253
                                                                                                                                                                                                                       STREET: 51 Uni-
CITY: Seattle
STATE: WA
PRIOR APPLICATION DATA: US/08/620,694
APPLICATION NUMBER: US/08/538,76
APPLICATION NUMBER: USSN 08/538,76
APPLICATION NUMBER: 7 AUGUST 1995
FILING DATE: 7 AUGUST 1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWIHPRNLTPSSPKDLQIQLHFAHTQOGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                COUNTRY:
                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (206
                                                                                                                                                                                                                                                                                                                                                                                  Application US/09022253
                                                                                                                                                                                                                                                   E: Immunex Corporation 51 University Street
                                                                                                                                                                                                                                                                                                                  Spriggs, Melanie
Fanslow, William
                                                                                                                                                                                                                                                                                                                                               yao, Zhengbin
                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1764; DB 3; 100.0%; Pred. No. 8.9e-177;
                 UMBER: USSN 08/538,765
7 AUGUST 1995
                                                                                                                                                                                                                                                                                                               No.
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                                                                                                                                                                                                                                                                                                             6096305el Receptor That Binds IL-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 866;
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RESULT 6
US-09-022-260-10
Sequence 10, Application US/09022260
Patent No. 6100235
                                                                                                               GENERAL INFORMATION:
APPLICANT: YAO, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Spriggs, Melanie
TITLE OF INVENTION: NO. 6100235el Receptor That Binds IL-17
CORRESPONDENCE ADDRESS:
ADDRESSE: Immunex Corporation
STREET: 51 University Street
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    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
CURRENT APPLICATION DATA:
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Best Local Similarity 100.
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TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                  241 ENHSCFEHMHIPADRDEEFHORSNVTLTLRNLKGCCRHOVOIOPFFSSCLNDCLRHSAT 300
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NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MGAARSPPSAVPGPILGILLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60
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APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
                                                                                                                                                                                                                                                                                                                                                  ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT
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US/09/022,260
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100.0%; Pr
*ative 0;
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Pred. No. 8.9e-177;
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US-09-022-259-10
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                                                                                                                                                                                                                                                                   Db.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Sequence 10, Application US/09022259
Patent No. 6191104
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Panslow, William
TITLE OF INVENTION: No. 6191104el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
COMPUTER READABLE FORM:
               Cli.
STATE: WA
COUNTRY: US
COUNTRY: 98101
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                                                             STREET: 51 Uni
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SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECHER TOPO
                                                                     ADDRESSEE: Immunex Corporation STREET: 51 University Street
                                                                                                                                                                                                                                                                                                              301 VSCPEMPDTPEPIPDYMPLW 320
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NAME: PECKINS, PACTICIA Anne
REGISTRATION NUMBER: 34,695
TELEPERENCE/DOCKET NUMBER: 2617-B
TELEPONGUNICATION INFORMATION:
TELEPONGUNICATION (206)587-0430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MGAARSPPSAVPGPLLGLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD
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"YPE: amino acid
"TOPOLOGY: linear
"MOLECULE TYPE: protein
US-09-022-259-10
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COMPUTER: Apple Power Macintosh
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.(
SOFTWARE: MICROSOft Word for Apple, Version 6.(
SOFTWARE: MICROSOft Word for Apple, Version 6.(
SOFTWARE: MICROSOft WORD APPLICATION NUMBER: US/09/022,259
APPLICATION NUMBER: US/09/022,259
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PRIOR APPLICATION DATA:
APPLICATION UNMER: US
APPLICATION UNMER: 23 MARCH
FILING DATE: 23 MARCH
CLASSIFICATION:
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US-09-022-257-10
US-09-022-257-10
Sequence 10, Application US/09022257
Sequence 10, Application US/09022257
Patent No. 6197525
Patent No. 1819784710N:
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 TNERLCVRFEFLSKLRHHRRWRETESHEVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240
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            APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
APPLICANT: Spriggs, Melanie
APPLI
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Immunex Corporation
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MOLECULE TYPE: protein US-09-022-257-10
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: anino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Apple Fower Macintosh
COMPUTER: Apple Fower Macintosh
COMPUTER: Apple Operating System 7.5.5
CORRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
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Best Local Similarity 100.
Matches 320; Conservative
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CITY: S
STATE:
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CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: USSN 08
APPLICATION NUMBER: 1995
APPLICATION NUMBER: 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617
TELECOMMUNICATION:
                                                    RESULT 9
US-08-620-694A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia
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Sequence 2, Application US/08620694A
Patent No. 5869286
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                             121 TNERLCVRFEBISKLRHHHRRWRETESHEVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
                                                                                                                                                                                                                                                                                                                61 SWIHPRNLTPSSPKDLQIQLHFAHTOOGDLFPVAHIEWTLOTDASILYLEGAELSVLQLN 120
                                                                                                                                                                                                                                                                                                                                                                    181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHOLKVSFTLWNESTHYOILLTSFPHM 240
                                                                                                                                                                                                                           181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHOLRVSFTLWNESTHYQILLISFPHM 240
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                                                                                                           VSCPEMPDTPEPIPDYMPLW -320
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                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 1764; DB 4;
100.0%; pred. No. 8.9e-177;
100.0%; pred. No. 8.9e-177;
tive 0; Mismatches 0;
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Query Match
Best Local Similarity '71.4'
Matches 230; Conservative
301 VPCPVISNTTVPKPVADYIPLW 322
                          301 VSCPEMPDT--PEPIPDYMPLW 320
                                                             241 ENHSCFEHMHHIPAPRPEDEHQRSNVTLTLRNLKGCCRHQVQIQPEFSSCLNDCLRHSAT 300
                                                                                           181 FVPDCEDSKMKMTTSCVSSGSLMDPNITVETLDTQHLKVDFTLWNESTPYQVILESFSDS 240
                                                                                                            181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240
                                                                                                                                                                      121 TNERLCVREEFLSKLRHHHRRWRETTESHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
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                                                                                                                                                    121 TNERĹĆVKFQFLSMÍQHHRKRWRFSFSHFVVDÞGQEYEVTVHHLÞKÞIÞDGDÞNHKSKII 180
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PILING DATE: 21 MARCH 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
PRIOR APPLICATION 435
PRIOR APPLICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/538,765
PRIOR APPLICATION 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                              61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120
                                                                                                                                                                                                                              61 SWIHPRNLTPSSPKDLQTQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: PETKINS, PATRICIA ANNE
REGISTRATION NUMBER: 34,695
TELECOMMUNICATION INFORMATION:
TELEPHONE: (20)587-0430
                                                                                                                                                                                                                                                                                         1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60
                                  ENHSCFDVVKQIFAPRQEEFHÖRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300
                                                                                                                                                                                                                                                                      1 MAIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
CURRENT APPLICATION DATA;
CURRENT APPLICATION DATA;
CURRENT APPLICATION DATA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UMBER: USSN 08/410,535
23 MARCH 1995
N: 435
                                                                                                                                                                                                                                                                                                                                           71.1%; Score 1254; DB 2;
71.4%; Pred. No. 3.8e-123;
ative 30; Mismatches 60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2617-B
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                                                                                                                                                                                                                                                                                                                                                                     Length 864;
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Query Match
Best Local Simi
Matches 230;
                                                                  US-09-022-255-2
                                                                                                                             TELEFAX: (206)
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                    MOLECULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-022-255-2
                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: USSN 08/620,694
FILING DATE: 21 MARCH 1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
PRIOR APPLICATION DATA: 70077 1995
PRIOR APPLICATION DATA: 70077 70 711 E35
                                                                                                                 LENGTH: 864 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09022255
Patent No. 6072033
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM
APPLE OPERATION SOFTWARE: Microsoft Word for Apple, Version 6.0.1
APPLICATION NUMBER: US/09/022,255
FILING DATE:
                                                                                               TOPOLOGY:
                                                                                                                                                                                                            NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 51 Univ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
ZIP: 98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: NO. 6072033el Receptor That Binds IL-17
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                                                                                                       amino acid
                                                                                                                                                                                                                                                                     DATE:
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                                                                              protein
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                                                                                                                                                                                                                                                          23 MARCH
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CH 1995
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241 ENHSCFDVVKQIFAPROEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300
                       241 ENHSCFEHMHHIPAPRPEEFHORSNVTLTLRNLKGCCRHOVOIOPFFSSCLNDCLRHSAT 300
                                                    181 FVPDCEDSKMKMTTSCVSSGSLMDPNITVETLDTOHLRYDFTLWNESTPYQVLLESFSDS 240
                                                                    181 LVPDCBHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240
                                                                                                     121 ÍNERLÓVKFOFLSMÍOHHRKRWRFSFSHFVVDÞGÓEYEVTVHHLPKPIPDGDÞNHKSKII 180
                                                                                                                     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIFDGDPNHQSKNF 180
                                                                                                                                                         61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120
                                                                                                                                                                         61 SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
                                                                                                                                                                                                             1 MAIRRCWPRVVPGPALGWELLLLNVLAPGRASPRELEDFPAPVCAQEGESCRVKNSTCLDD 60
                                                                                                                                                                                                                         1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60
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Similarity 71.1%; Score 1254; DB 3;
30; Conservative 30; Mismatches 60;
                                                                                                                                                                                                                                                                                              Length 864;
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RESULT 11 US-09-022-696-2

sequence 2, Apr patent No. 6072

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241 ENHSCFEHMHHIPAPRPEBEHQRSNVTLTLRNLKGCCRHQVOIQPEFSSCLNDCLRHSAT 300

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GENERAL INFORMATION:
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APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
APPLICANT: Fanslow, William
APPLICANT: Fanslow, William
APPLICANT: Sanskown William
APPLICANT: Sanskown William
APPLICANT: Springs William
APPLICANT: Springs William
APPLICANT: Springs William
APPLICANT: Yao, Zhengbin
APPLICANT: Yao, Zhengb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA

COUNTRY: SAIO1

ZIF: 98101

COMPUTER READABLE FORM:

COMPUTER: Floppy disk

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

COMPUTER: Apple Operating System 7.5.5

COMPUTER: Apple Operating System 6.0.1

COPTWARE: Microsoft Word for Apple, Version 6.0.1

SOFTWARE: MICROSOft Word for Apple, Version 6.0.1

CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                         Query Match 71.48; Best Local Similarity 71.48;
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 51 Uni
                                                                                                                                                                                                                                                                         Matches 230;
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Immunex Corporation STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VPCPVISNTTVPKPVADYIPLW 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REGISTRATION NUMBER: 2617
REFERENCE/DOCKET NUMBER: 2617
REFERENCE/DOCKET INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/022,696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
CLASSIFICATION DATA:
RIOR APPLICATION NUMBER: USSN 0:
APPLICATION NUMBER: 1995
FILING DATE: 23 MARCH 1995
FILING DATE: 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/09022696
5072037
                                                      121 TNERLCVRFEELSKLRHHRRWRETESHFVVDPDQEYEVTVHHLEKPIEDGDPNHOSKNF 180
                                                                                                                                                   61 SWIHPRNLTPSSPKDLQIOLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQIN 120
                                    121 TNERLCVKFOFLSMLOHHRKRWRESESHEVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180
                                                                                                                                                                                            61 SWIHPKNLTPSSPKNIYINLSVSSTOHGELYPVLHYEWTLOTDASILYLEGAELSVLOLN 120
LVPDCEHARMKVTTPCMSSGSLMDPNITVETLEAHQLRVSETLWNESTHYQILLTSEPHM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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pred. No. 3.8e-123;
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US-08-978-773-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08978773
Patent NO. 6083906
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 ENHSCFDVVKQIFAPROEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein US-08-978-773-2
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CORRESPONDENCE ADDRESS:
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Best Local Similarity
Matches 230; Conserv
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INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/978,773 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Perkins, Patricia
REGISTRATION NUMBER: 34,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
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                                                                                                                                            121 TNERLCVREBELSKLRHHHRRWRETESHEVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98101
                                                                               181 LVPDCEHARMKVTTPCMSSGSLMDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240
                                                                                                                                                                                                       61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120
                                                                                                                                                                                                                           61 SWIHPRNLTPSSPKDLQIQLHEAHTQQGDLEPVAHIEWTLQTDASTLYLEGAELSVLQLN 120
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111arity 71.4%; Pred. No. 3.8e-123;
Conservative 30; Mismatches 60;
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Length 864; Indels

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RESULT 13 US-09-022-253-2

Sequence 2, Patent No.

APPLICANT: APPLICANT: APPLICANT:

COUNTRY: US ZIP: 98101

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WOLECULE TYPE: Protein
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                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694
FILING DATE: 21-MARCH-1996
FILING DATE: 7 AUGUST 1995
                                        61 SWIHPRNLTPSSPRDLQIQLHFAHTQQSDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 23 MARCH
                                                                 1 MAIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60
                                                                                  1 MGAARSPPSAVPGPLLGLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60
                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: PERKIDS, Patricia &
REGISTRATION NUMBER: 34,6
                                                                                                                                                                                                                                                                                                                 REGISTRATION UNMBER: 34,695
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206,587-0470N:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
SOFTWARE: Microsoft Word Operating System 7.5.5
APPLICATION DATA:
FILING DATE: US/09/022,253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 51 CITY: Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Immunex Corporation STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 VPCPVISNTTVPKPVADYIPLW 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 VSCPEMPDT--PEPIPDYMPLW 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 FVPDCEDSKMKWTTSCVSSGSLWDDNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240
                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENHSCEDVVKQIFAPRQEEFHORANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300
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71.4%; Pred. No. 3.8e-123;
itive 30; Mismatches 60;
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CH 1995
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                                                                                                                                               Length 864;
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                                                                                  TOPOLOGY: 11

MOLECULE TYPE:
US-09-022-260-2
            Query Match
Best Local Similarity 71.1
Matches 230; Conservative
                                                                                                              INFORMATION FOR SEQ ID NO.
SEQUENCE CHARACTERISTICS.
LENGTH: 864 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                           NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
TYPICHUMTON.
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US-09-022-260-2
                                                                                                                                                                                                                                     NAME: Perkins Date:
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APPLICATION NUMBER: 08/620,694
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ADDRESSEE: Immunex Corporation
STREET: 51 University Street
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STREET: 51 CITY: Seattle
~~ATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17
                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
ZIP: 98101
                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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71.1%; Score 1254; DB 3;
71.4%; Pred. No. 3.8e-123;
tive 30; Mismatches 60;
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US-09-022-259-2
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Patent No. 6191104
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                   TELEPAX: (206)
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
TYPE: amino acid
                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/410,535

APPLICATION NUMBER: USSN 08/410,535

FILING DATE: 23 MARCH 1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695

REFERENCE/DOCKET NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:

TOTAL TRATTON OF TATALOGUE

TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
COMPUTER: Apple Power and System 7.5.5
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0
CURRENT APPLICATION NUMBER: US/09/022,259
APPLICATION NUMBER: US/09/022,259
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APPLICATION NUMBER:
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Immunex Corporation STREET: 51 University Street CITY: Seattle
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Best Local Similarity 71.4%;
Matches 230; Conservative 3
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301 VPCPVISNTTVPKPVADYIPLW 322
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                                        ENHSCFEHMHHIPAPRPEEFHORSNYTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300
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Pred. No. 3.8e-123;
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Copyright (c) 1993 - 2000
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95US-0410535.
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Protein; 866

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ALIGNMENTS

Amino acid sequenc Novel protein kina Human IPV-gamma ac Human lysosomal me Human lysosomal me

Location/Qualifiers

/label= Sig_peptide 28..320 28..320 /label= Extracellular_domain

/label= Transmembrane_domain 342..866

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/label= Cytoplasmic_tail

96WO-US04018

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
                                                                           Interleukin-17 receptor; IL-17 receptor; human; nitric oxide;
cartilage; osteoarthritis; autoimmune disease; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                           Homo sapiens.
                            Peptide
                                                                                                                     Human interleukin-17 receptor.
                                                                                                                                                  12-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                      AAW61272 standard; Protein; 866
                                                                                                                                                                           AAW61272;
                                                                                                                                                                                                                                             301 vscpempdtpepipdymplw 320
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                                                                                                                                                                                                                                                                                                                        241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The human interleukin-17 receptor (IL-17R) (AAW04184) is a type I transmembrane protein. Its amino acid sequence was deduced from a cDWA clone (AAT33801) isolated from a human peripheral blood lymphocyte library. Soluble, recombinant forms of the receptor (Partic. amino acids 1-320) can be prepd. in transformed host cells and used to regulate immune and inflammatory responses, in methods for suppressing rejection of grafted organs or tissue, and in assays of IL-17 and IL-17R.
                                                                                                                                                                                                                                                                                                                                  181 LVPDCEHARMKYTTPCMSSGSLWDPNITVETLEAHOLRVSETLWNESTHYQILLTSFPHM 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding interleukin-17 receptor - useful for regulating immune and inflammatory responses, or to suppress graft rejection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fanslow WC,
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                                                                                                                                                                                                                                                        VSCPEMPDTPEPIPDYMPLW 320
                                                                                                                                                                                                                                                                                      ENHSCFEHMHHIPAPRDEEFHQRSNVTLTLRNLKGCCRHQVQIQPEFSSCLNDCLRHSAT 300
                                                                                                                                                                                                                                                                            enhscfehmhnipapr\\peefhqrsnvtlitlrnlkgccrhqvqlqpffssclndclrhsat
                                                                                                                                                                                                                                                                                                                        lvpdceharmkvttpcmssgslwdpnitvetleahglrvsftlwnesthygilltsfphm
                                                                                                                                                                                                                                                                                                                                                                   tnerl cvrfeflsklrhhhrrwrftfshfvvdpdqeyevtvhhlpkpipdgdpnhqsknf
                                                                                                                                                                                                                                                                                                                                                                             TNERLCVREEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
                                                                                                                                                                                                                                                                                                                                                                                                             swihprnltpsspkdlqiqihfahtqqqdifpvahiewtlqtdasilylegaeisvlqln 120
                                                                                                                                                                                                                                                                                                                                                                                                                        SWIHPRNLIPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1996-443184/44.
DB; AAT33801.
                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            866 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11arity 100.0%; Score 1764; DB 17; Length 866; Conservative 0; Mismatches - 1764; DB 17; Length 866;
/label= Sig_peptide
28..866
                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spriggs MK,
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                                                                                                                                                                                                                                                                                                                          This polypeptide comprises human full-length interleukin-17 CC receptor (IL-17R). A claimed method for reducing the amount of CC receptor (IL-17R). A claimed method for reducing the amount of CC contacting the cell with a soluble II-17R, especially claimed CC contacting the cell with a soluble II-17R, especially claimed CC peptide and extracellular domains of the respective full-length CC receptors. Recombinant soluble IL-17R polypeptides can be obtained CC using prokaryotic or eukaryotic (for glycosylated products) CC expression systems. A cDMA sequence coding for full-length human CC initric oxide production from cartilage-associated cells in CC individuals with osteoarthritis. Inhibitors of nitric oxide production, such as soluble II-17R, may therefore be useful to CC amellorate the effects of nitric oxide in osteoarthritis as well as a suntainmune and inflammatory diseases.
                                                                                                                                                                                                                                                                               Query Match
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241 ENHSCFEHMHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT
                                                 181
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                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                      61
                                                                                                                                                                             Claim 2(b); Page 27-31; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reducing nitric oxide production by cartilage associated cells -contacting cells with soluble interleukin-17 receptor, useful to treat osteoarthritis and autoimmune and inflammatory diseases
                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-322457/28.
N-PSDB; AAV27592.
                                      LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHOLRVSFTLWNESTHYQILLTSFPHM
                                                                         TNERLCVRFEELSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IMMV ) IMMUNEX CORP.
                         {\tt lvpdceharmkvttpcmssgslwdpnitvetleahqlrvsftlwnesthyqilltsfphm}
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                                                                                                                                                                                                                                                     320;
                                                                                                                                                                                                                                                                                                                  866 AA;
                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                        100.0%;
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/note= "Claim 2(b)"
28..320
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                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                      Score 1764; DB 19;
Pred. No. 1.7e-169;
); Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IL-17R; human; interleukin-17 receptor; immunoregulator; inhibitor; T cell proliferation; T cell activation; organ; graft; rejection; T cell proliferation; allergy; asthma; treatment; inflammatory disease; autoimmune disease; allergy; asthma; treatment; inmunogen.

B cell proliferation; immunoglobulin secretion; immunogen.
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23-MAR-1995;
07-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
                                Query Match
Best Local Similarity
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                         Matches
                                                                                                  This sequence represents a human interleukin-17 receptor (II-17R).

IL-17R polypeptides have immunoregulatory activity. They can be used for inhibiting T cell activation. In inhibiting T cell proliferation, or for inhibiting T cell activation. In particular they can be used for preventing or treating organ or graft rejection, autoimmune disease, allergy or asthma. They can also be used for the prevention or treatment of inflammatory disease in which activated T cells play a role or for inhibiting B cell proliferation or immunoglobulin secretion. The II-17 polypeptides can also be used as immunogens, reagents in in vitro assays, or as binding agents for affinity purification procedures.
                                                                                                                                                                                                                                                           Isolated interleukin-17 receptor DNA - used to develop products for treating e.g. organ or graft rejection, autoimmune disease, allergy, asthma or inflammatory disease
                                                                                                                                                                                                                                                                                                                                                                      (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                Fanslow WC,
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                                                                                                                                                                                                                                       Disclosure; Column 43-48; 25pp; English.
                                                                                 Sequence
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1 MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60
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95US-0410535.
95US-0538765.
                           100.0%;
ilarity 100.0%;
Conservative (
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28..866
/label= IL-17R
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                                  0;
                                Score 1764; DB 20;
pred. No. 1.7e-169;
prismatches 0;
                                           Indels
                                                             Length
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                                                                                                                                                                                                                                                   IL-17R;
murine;
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                                                                                                                                                                                                                                                                    Human IL-17R protein.
                                                                                                                                                                                                                                                                                  10-JAN-2001
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                                                                                                                                                                                                                peptide
                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                     Domain
                                                                                    21-MAR-1996;
23-MAR-1995;
07-AUG-1995;
                                                                                                                                                                           Domain
                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
                                                                                                                                                                                                                                                                                                                                                                                                                        TNERLCYRFEFLSKLRHHRRWRFTFSHFYVDDDQEYEVTYHHLPKPIPDGDPNHQSKNF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWIHDRNILTESSPKDLQIQLHEAHTQQGDLFPVAHIEWTLQTDASILYL5GAELSVLQLN 120
                                                                                                                                         US6072037-A.
                                                                                                                                                                                                                                                                                                                                                                                               12-FEB-1998;
                                                                                                                             06-JUN-2000
           Antibodies immunoreactive with interleukin-17 receptor protein useful in interfering with receptor binding to CTLA-8, as components of in interfering with receptor binding to Harden as a diagnostic or research assays or in affinity purification of the diagnostic or research assays or in affinity purification.
                                                                       (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                         4
                                        WPI; 2000-411206/35.
N-PSDB; AAA61240.
                                                           Fanslow WC,
                                                                                                                                                                                                                                                                                                                                                 VSCPEMPDTPEPIPDYMPIW 320
                                                                                                                                                                                                                                                                                                                                            vscpempdtpepipdymplw
                                                                                                                                                                                                                                                  CTLA-8; interleukin 17; Herpesvirus saimiri; HVS antibody; immune suppression.
                                                                                                                                                                                                                                                                                    (first entry)
                                                             Spriggs
                                                                                       96US-0620694.
95US-0410535.
95US-0538765.
                                                                                                                  98US-0022696
                                                                                                                                                        /label= Cytoplasmic_domain
32..866
/label= IL-17R
                                                                                                                                                                             /label= Transmembrane_domain 342..866
                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                             /label=
                                                                                                                                                                                                  /label=
                                                                                                                                                                                                                                                                                                               protein; 866
                                                                XX,
                                                                                                                                                                                                               Signal_peptide
                                                                                                                                                                                                  Extracellular_domain
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RESULT

AAY 97131

ID AAY 9

XX AAY 9

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              Domain
                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a novel receptor that binds Interleukin CC (II-17, also known as CTLA-8) and a Herpesvirus saimiri homolog, CC HVS13. The receptor is a type I transmembrane protein which is referred as II-17R. Murine thymona EL4 (cells were found to express a component of a cDNA encoding the receptor was identified. The murine II-17R cDNA encoding the receptor was identified. The murine II-17R cDNA collate DNA encoding human II-17R by cross species hybridisation. The cDNA was used to creceptor may be used to regulate immune responses, for example to creceptor may be used to regulate immune responses, for example to cuseful as components of diagnostic or research assays. Such antibodies components of diagnostic or research assays. Such antibodies was also be used in affinity purification of the receptor.
                                                                                 Protein
                                                                                                                     Peptide
                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                    IL-17R; interleukin-17 receptor; soluble; CTLA-8; Herpesvirus saimiri;
HSV13; graft rejection; suppressor; immunosuppressive; anti-allergic;
                                                                                                                                                                                                                                                                   Human interleukin-17 receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSCPEMPDTPEPIPDYMPLW 320
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  Soluble_IL-17_receptor
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                                301 VSCPEMPDTPEPIPDYMPLW 320
301 vscpempdtpepipdymplw
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                                                                                                                                                                                                                                181 LVPDCEHARMKYTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A novel interleukin-17 receptor (IL-17R) was identified by screening a cDNA library from T cell thymoma EL4 cells, which were identified as binding fusion proteins comprising human immunoglobulin G1 (IGG1) Fc region and soluble IL-17 (CTLA-8) protein or a homologous Herpesvirus saimiri (HSV) protein, designated HSV13. Regulating an murine IL-17R. Soluble IL-17R fragments comprises administering extracellular domain that bind IL-17R imman IL-17R, and fragments comprises the an immunoresponse, for treating or preventing diseases like allergy, assistant and autolimnune diseases, and for suppressing rejection of grafted company of the suppression of the 
                                                                                                                                                                                                                                                                                                                 121 tnerlcvrfefiskirhhhrrwrftfshfvvdpdqeyevtvhhlpkpipdgdpnhqsknf
                                                                                                                                                                                                                                                                                                                                              121 TNERLCVRFEEFLSKLRHHHRRWRETFSHFVVDEDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAR-1996;
23-MAR-1995;
07-AUG-1995;
                                                                       WPI; 2000-548298/50.
N-PSDB; AAA51988.
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95US-0410535.
95US-0538765.
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                                                               CC CDNA library from T cell thymoma EL4 cells, which were identified as CC condition fusion proteins comprising human immunoglobulin Gl (IGG1) FC CC binding fusion proteins comprising human immunoglobulin Gl (IGG1) FC CC rejection of a grafted syngeneic or allogeneic organ or tissue in a graft CC rejection of a grafted syngeneic or allogeneic organ or tissue in a graft CC rejection of a grafted syngeneic or allogeneic organ or tissue in a graft CC with DNA encoding soluble IL-17R, so that expression of IL-17R by the CC with DNA encoding soluble il-17R, so that expression of rejection. Soluble CC engrafted organ or tissue results in suppression of rejection. Soluble CC IL-17R fragments comprise residues 1-322 of the murine IL-17R, residues CC IL-17R fragments comprise residues 1-320 of the surfue of the surfue of suppressing rejection of grafted organs or tissues in the recipient CC and for treating or preventing diseases like allergy, asthma and CC and for treating or preventing diseases like allergy, asthma and CC and for treating or preventing diseases like allergy, asthma and
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HSV13; graft rejection; suppressor; immunosuppressive; anti-allergic;
anti-asthmatic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Suppressing rejection of a grafted syngeneic or allogeneic organissue in a graft recipient for organ transplantation involves transfecting the organ or tissue with DNA encoding soluble interleukin-17 receptor
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N-PSDB; AAA52146.
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                                                          autoimmune
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23-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                        07-AUG-1995;
This invention relates to an isolated and purified interleukin-17 receptor (IL-17R). A soluble IL-17 protein (CTLA8) and a herpesvirus stamiri (HVSI3) open reading frame (homologous to CTLA8) were expressed as fusion proteins comprising an immunoglobulin Fc region, and used to
                                                                                                                                           Interleukin-17 receptor protein useful for regulating immune and for preventing or treating organ or graft rejection, auto disease, allergy or asthma in human .
                                                                                                                                                                                                                               WPI; 2000-411205/
N-PSDB; AAA59871.
                                                                                                                                                                                                                                                                                           Fanslow WC,
                                                                                                                                                                                                                                                                                                                                (IMMV ) IMMUNEX CORP
                                                                                                       Claim 1; Column
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vscpempdtpepipdymplw 320
                                                                                                                                                                                                                                                     2000-411205/35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                               Spriggs
                                                                                                                                                                                                                                                                                                                                                                             96US-0620694.
95US-0410535.
95US-0538765.
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                                                                                                                43-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                   26pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1764; DB 21;
pred. No. 1.7e-169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                     English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A
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                                                                                                                                                                                                autoimmune
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11-FEB-1998;
                                        06-MAR-2001.
                                                                            US6197525-B1
                                                                                                                                             Domain
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Best Local Similarity
                                                                                                                                                                                 Domain
                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                      CTLA-8;
                                                                                                                                                                                                                                                                                                                                                                                              immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB62066 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB62066;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     screen for the expression of the IL-17R. The screening identified the novel receptor of the invention. IL-17R is a type I transmembrane protein that exhibits antiinflammatory, immunosuppressive, antiasthmatic and antiallergic activities, and is an inhibitor of T cell proliferation dectivation. IL-17R can be used to regulate immune functions, and is useful for preventing or treating organ or graft rejection, autoimmune interleukin-17 receptor amino acid sequence represents the human interleukin-17 receptor amino acid sequence identified in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSCPEMPDTPEPIPDYMPLW 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interleukin-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                       (hCTLA-8 receptor) polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               866 AA;
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                                                                                                                                                                           /note=
321..3
                                                                                                                                      /note=
342..8
                                                                                                                                                                                                               28..320
                                                                                                                                                                                                                                                        /note= "signal peptide" 28..866
                                                                                                                                                                                                                                  note=
                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                       n-17; IL-17; IL-17 receptor; IL-17R; human; antiallergic; antiasthmatic; antiinflammat
                                                                                                                       .341
te= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                             "extracellular domain"
                                                                                                                                                                                                                     "mature protein"
                                                                                                      "cytoplasmic domain"
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                                                                                                                                                                                                                                                                                                                                                                     antiinflammatory.
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Best Local S
Matches 320
Human; Interleukin-17 receptor; IL-17R; immunosuppressive; antiasthmattc; antiinflammatory; graft rejection; autoimmun inflammatory disease; allergy; CTLA-8; immunogen; asthma.
                                                    Human
                                                                                                             AAY72754 standard;
                                                                                                                                                           241
                                                                                                                                                                                                                               241
                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention is directed towards assays for detection of interleukin-17 (IL-17), IL-17 receptor (IL-17R), and (antagonists or mimetics of) the interaction between IL-17 and IL-17R. The assay kit comprises an IL-17R and a detecting reagent. The method is useful for inhibiting useful for preventing or treating organ or graft rejection, autoimmune diseases, allergy, asthma and inflammatory diseases in which activated human IL-17R (hCTLA-8 receptor) polypeptide.
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                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Columns 37-44; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New assay kits for detecting interleukin-17 (IL-17), IL-17 receptors and (antagonists or mimetics of) the interaction between IL-17 and IL-17 receptor, useful for treating autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-1996;
23-MAR-1995;
07-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 320; Conserv
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                                                                                                                                                                                            Interleukin-17
                                                                                                                                                                                                                                             LVPDCEHARMKVTTPCMSSGSLMDPNITVETLEAHQLRVSFTLMNESTHYQILLTSFPHM
                                                                                                                                                                                                                                                                           {\tt lvpdceharmkvttpcmssgslwdpnitvetleahqirvsftlwnesthyqilltsfphm}
                                                                                                                                                                                                                                                                                                                              SWIHPRNITPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
                                                                                                                                                                                                                                                                                                                                                          MGAARSPDSAVPGPLLGLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60
                                                                                                                                                                                                                                                                                                                    swihprnitpsspkdlqiqlhfahtqqqdlfpvahiewtlqtdasilylegaelsvlqln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-234480/24.
DB; AAF57188.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spriggs MK,
                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   866 AA;
                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96US-0620694.
95US-0410535.
95US-0538765.
                                                                                                            Protein;
                                             receptor
                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fanslow
                                                                                                            866
                                       (IL-17R) or CTLA-8 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1764; DB 22;
Pred. No. 1.7e-169;
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          autoimmune
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                antiallergic;
                                                                                                                                                                                                                                                                                                                                                                                                                           866;
                                                                                                                                                                                                                                                                                                                                                                                                       0,
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The present sequence is human Interleukin-17 receptor (IL-17R) or CC CTLA-8 receptor. Human IL-17R is isolated from a human peripheral CC CTLA-8 receptor. Human IL-17R is isolated from a human peripheral CC Imphocyte library by cross-species hybridisation.

CC Diood lymphocyte library by cross-species hybridisation. The invention relates to Interleukin-17 receptors (IL-17R), and their corresponding nucleic acid molecules. IL-17R is CC response. The invention is useful for suppressing rejection of a grafted CC argues. The invention is useful for suppressing rejection of a grafted CC response. The invention is useful for suppressing rejection of a grafted CC argues in a graft recipient. Soluble IL-17 (CTLA-8) receptors CC argues of itssue in a graft recipient. Soluble IL-17 fusion proteins argues of activated T-cells play a role. Soluble IL-17 fusion proteins argues of IL-17 activated T-cells play a role. Soluble IL-17 receptor. Derivatives of IL-17R CC argues of IL-17 receptor. Derivatives of IL-17R argues of IL
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23-MAR-1995;
07-AUG-1995;
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                                                                                                                                                                                                                                                                           Query Match
Best Local
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                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spriggs MK, Fanslow WC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Suppressing rejection of grafted organ or tissue in graft recipient, involves administering to recipient a composition comprising interleukin 17 receptor protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAD02815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Column 43-48; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens.
181 LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM 240
                                                                                                                                                 61
                                                                                                                                                                               2001-217901/22
                                    TNERLCVRFEFLSKLRHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
                                                                                                       al Similarity
320; Conserv
                                                                                                                                                                                                                                                                                                                                                           866 AA;
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95US-0410535.
95US-0538765.
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                                                                                                                                                                                                                                                                                   100.0%; Score 1764; DB 22; 100.0%; Pred. No. 1.7e-169;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IL-17R, interleukin-17 receptor; soluble; CTLA-8; Herpesvirus saimiri; HSV13; graft rejection; suppressor; immunosuppressive; anti-allergic; anti-asthmatic; Flag epitope; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Soluble IL-17R/Flag fusion protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY97255;
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                                                                                                                                                                                                                                                                                                                                                                                           11-FEB-1998;
A novel interleukin-17 receptor (IL-17R) was identified by screening a cDNA library from T cell thymnoma EL4 cells, which were identified as binding fusion proteins comprising human immunoglobulin Gl (IgG1) FC binding fusion proteins comprising human immunoglobulin Gl (IgG1) FC protein or a homologous region and soluble IL-17 (CTLA-8) protein or a homologous rejection of a grafted syngeneic or allogeneic organ or tissue in a rejection of a grafted syngeneic or allogeneic organ or tissue to be graft recipient involves transfecting the organ or tissue to be transplanted with DNA encoding soluble IL-17R, so that expression of transplanted with DNA encoding soluble results in suppression of transplanted with DNA encoding soluble il-17R, and fragments of the murine IL-17R, residues 1-320 of the human IL-17R, and fragments of the extracellular domain that bind IL-17. The method is useful for regulating extracellular domain that bind IL-17. The method is useful for regulating
                                                                                                                                                                                          suppressing rejection of a grafted syngeneic or allogeneic organ tissue in a graft recipient for organ transplantation involves transfecting the organ or tissue with DNA encoding soluble interleukin-17R receptor
                                                                                                                                                                                                                                                                                                                                        07-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                    21-MAR-1996;
23-MAR-1995;
                                                                                                                                                                                                                                                                                      Fanslow WC,
                                                                                                                                                                                                                                                                                                           (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                              WPI; 2000-523862/47
                                                                                                                                                                    Example 3; Column -; 27pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                        Spriggs MK,
                                                                                                                                                                                                                                                                                                                                         96US-0620694.
95US-0410535.
95US-0538765.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label=
32..322
                                                                                                                                                                                                                                                                                                                                                                                             98US-0022253
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323..330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Soluble_IL-17_receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Flag_epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IL-17_receptor_extracellular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal_peptide
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   21-MAR-1996;
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                                              08-AUG-2000
                                                               US6100235-A
                                                                                            Peptide
                                                                                                           Protein
                                                                                                                             Peptide
                                                                                                                                                                        IL-17R; interleukin-17 receptor; soluble; CTLA-8; Herpesvirus saimiri
HSV13; graft rejection; suppressor; immunosuppressive; anti-allergic;
anti-asthmatic; Flag epitope; fusion protein.
                                                                                                                                               Protein
                                                                                                                                                                                                                   Soluble IL-17R/Flag fusion protein.
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                                                                                                                                                                                                                                           04-DEC-2000
                                                                                                                                                                                                                                                                        AAY97258 standard; peptide;
                                                                                                                                                                                                                                                                                          258
                                                                                                                                                                                                                                                                                                                    301 vpcpvisnttvpkpvadyiplw
                                                                                                                                                                                                                                                                                                                                           301
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                                                                                                                                                                                                                                                                                                                                                                                                             181 LVPDCEHARMKYTTPCMSSGSLWDPNITVETLEAHOLRVSETLWNESTHYOILLTSEPHM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   an immunoresponse, for suppressing rejection of grafted organs or tissues in the recipient and for treating or preventing diseases like allergy, asthma and autoimmune diseases.

Note: This sequence does not appear in the specification. It was created from the full length murine IL-17R (see AAY97180) and the flag peptide (see AAY97183)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
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                                                                                                                                                                                                                                                                                                                                                     ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300
                                                                                                                                                                                                                                                                                                                                            enhscfdvvkqifaprqeefhqranvtftlskfhwcchhhvqvqpffssclndclrhavt
                                                                                                                                                                                                                                                                                                                                                                                                                                                  {\tt swihpknltpsspkniyinlsvsstqhgelvpvlhvewtlqtdasilylegaelsvlqln}
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
96US-0620694
95US-0410535
                                                                                                                                                                                                                                        (first
                         98US-0022260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                       /label= Flag_epitope
                                                                                   /label=_IL-17_receptor_extracellular_domain
                                                                                                      /label= Signal_peptide
32..322
                                                                                                                          /label- Soluble_IL-17_receptor
                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                       entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71.1%; Score 1254; DB 21; 71.4%; Pred. No. 1.7e-118; tive 30; Mismatches 60;
                                                                                                                                                                                                                                                                         330
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CC A novel interleukin-17 receptor (IL-17R) was identified by screening a CC cDNA library from T cell thymona EL4 cells, which were identified as CC tegion and soluble IL-17 (CTLA-8) protein or a homologous (IGG1) FC CC Herpesvirus saimiri (HSV) protein, designated HSV13. Regulating an CC soluble IL-17R. Soluble IL-17R fragments comprises administering an CC soluble IL-17R. Soluble IL-17R fragments comprises residues 1-320 of the murine IL-17R, residues 1-320 of the human IL-17R, and fragments of the CC extracellular domain that bind IL-17. The method is useful for CC regulating an immunoresponse, for treating or preventing diseases like CR rafted organs or tissues in the recipient. Sequence does not appear in the specification. It was created CC from the full length murine IL-17R (see AAY97130) and the flag peptide XXX.
     Sequence
                                                                                                                                                                                                                                                                                                                               Regulating, treating or preventing immune or inflammatory response in mammal, especially organ or graft rejection, allergy or asthma, comprises administering interleukin-17 receptors
                                                                                                                                                                                                                                                                                                               Example 3; Column -; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-548298/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fanslow WC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-AUG-1995; 95US-0538765.
330 AA;
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AAW04184
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                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 71.1
Best Local Similarity 71.4
Matches 230; Conservative
Interleukin-17
                Murine interleukin-17 receptor.
                                            05-DEC-1996
                                                                   AAW04184;
                                                                                 AAW04184 standard; Protein;
                                                                                                                                                 301
                                                                                                                                                                       241 ENHSCFEHMHHIPAPRPEEFHORSNVTLTLRNLKGCCRHQVOIQPFFSSCLNDCLRHSAT
||||||: | ||| ||||||||||
241 enhscfdvvkqifaprqeefhqranvtftlskfhwcchhhvgvqpffssclndclrhavt
                                                                                                                                                                      301
                                                                                                                                                                                                                  181 fvpdcedskmkmttscvssgslwdpnitvetldtqhlrvdftlwnestpyqvllesfsds
                                                                                                                                                                                                                                181 LVPDCEHARMKYTTPCMSSGSLWDPNITVETLEAHOLRVSETLWNESTHYQILLTSEPHM
                                                                                                              . 12
                                                                                                                                                                                                                                                                           121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                    vpcpvisnttvpkpvadyiplw 322
                                                                                                                                                   VSCPEMPDT--PEPIPDYMPLW 320
                                                                                                                                                                                                                                                              swihpknitpsspkniyinlsvsstqhgelvpvlhvewtiqtdasilylegaelsvlqin
                                                                                                                                                                                                                                                                                                                      SWIHPRNLTESSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                        71.1%; Score 1254; DB 21; 71.4%; Pred. No. 1.7e-118; tive 30; Mismatches 60;
                                                                                 864 AA
                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 330;
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receptor; IL-17R; autoimmune disease;

allergy;

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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-AUG-1995;
23-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09629408-A1
                                                                                                                                                                                                                                                                       The murine interleukin-17 receptor (IL-17R) (AAW04184) is a type I transmembrane protein that binds IL-17 (CTLA-8, see also AAW02386) and HVS13 (AAW02387), a viral homologue of IL-17. Its amino acid sequence was deduced from a cDNA clone (AAT33800) isolated from murine thymoma EL4 cells. Soluble, recombinant forms of the receptor (partic. amino acids 1-322) can be prepd. in transformed host cells and used to regulate immune and inflammatory responses, in methods and used to regulate immune and inflammatory responses, and in for suppressing rejection of grafted organs or tissue, and in assays of IL-17 and IL-17R.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Fanslow WC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 29-32; 52pp; English.
                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                      encoding interleukin-17 receptor - useful for regulating immune inflammatory responses, or to suppress graft rejection
                                                     Local Similarity
                                                                                              121
                                                                                                                                                     61
                                                                                                                                   61
                                                                                                                                                                    1 MGAARSPPSAVPGPLLGLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD 60
                                                                                                                                                                                                                                                                                                                                                                                                                              1996-443184/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  graft rejection; inflammation; cytokine; therapy.
                                                                                                                                TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
                   230;
   VSCPEMPDT -- PEPIPDYMPLW 320
                                                                                                                                                                                                                                                                                                                                                                                                                    AAT33800
                                                                                                                                                                                                                                                           864 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Spriggs MK,
                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-0538765.
95US-0410535.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                323..343
/label= Transmembrane_domain
344..864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Sig_peptide
32..322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Cytoplasmic_tail
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Extracellular_domain
                                                                                                                                                                                                                        71.18; 71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yao
                                                                                                                                                                                                                 30;
                                                                                                                                                                                                               score 1254; DB 17;
pred. No. 6.7e-118;
0; Mismatches 60;
                                                                                                                                                                                                                                      Length 864;
                                                                                                                                                                                                                     Indels
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AAW61271

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                  This polypeptide comprises mouse full-length interleukin-17 cc receptor (IL-17R). A claimed method for reducing the amount of cnitric oxide produced by a cartilage associated cell comprises cc nitric oxide produced by a cartilage associated cell comprises contacting the cell with a soluble IL-17R, especially claimed contacting the cell with a soluble IL-17R, especially claimed contacting the cell with a soluble IL-17R, especially claimed contacting the signal cc receptors. Recombinant soluble IL-17R polypeptides can be obtained cc using prokaryotic or eukaryotic (for glycosylated products) cc expression systems. A cDNA sequence (see AAV27591) coding for altric oxide production from cartilage-associated cells in fittic oxide production from cartilage-associated cells in fittic oxide production, such as soluble IL-17R, may therefore be useful to production, such as soluble IL-17R, may therefore be useful to cardinate the effects of nitric oxide in osteoarthritis as well can other disease conditions in which nitric oxide plays a role, c. g. autoimmune and inflammatory diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW61271 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse interleukin-17 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW61271;
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301 vpcpvisnttvpkpvadyiplw
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Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interleukin-17 receptor; IL-17 receptor; mouse; nitric oxide; cartilage; osteoarthritis; autoimmune disease; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Domain
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N-PSDB; AAV27591.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reducing nitric oxide production by cartilage associated cells contacting cells with soluble interleukin-17 receptor, useful to treat osteoarthritis and autoimmune and inflammatory diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2(a); Page 20-23; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Soluble_IL-17R
/note= "Claim 2(a)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'label=
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SO

Sequence

864 AA;

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AAW92408
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                                                                                                                                                                                                                                                                                                                                                                                                                      Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                        Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
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                                                                                                     21-MAR-1996;
23-MAR-1995;
07-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
Isolated interleukin-17 receptor DNA - used to develop products for treating e.g. organ or graft rejection, autoimmune disease, allergy,
                                       WPI; 1999-152766/13.
N-PSDB; AAX01921.
                                                                   Fanslow WC,
                                                                                  (IMMV ) IMMUNEX CORP.
                                                                                                                                        21-MAR-1996;
                                                                                                                                                           09-FEB-1999
                                                                                                                                                                          US5869286-A.
                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                        IL-17R; murine; interleukin-17 receptor; immunoregulator; inhibitor; T cell proliferation; T cell activation; organ; graft; rejection; autoimmune disease; allergy; asthma; treatment; inflammatory disease; B cell proliferation; immunoglobulin secretion; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                 Murine IL-17R protein.
                                                                                                                                                                                                                                                                                                                      21-APR-1999
                                                                                                                                                                                                                                                                                                                                         AAW92408;
                                                                                                                                                                                                                                                                                                                                                 AAW92408 standard; Protein; 864 AA
                                                                                                                                                                                                                                                                                                                                                                                          301 vpcpvisnttvpkpvadyiplw 322
                                                                                                                                                                                                                                                                                                                                                                                                       301 VSCPEMPDT--PEPIPDYMPLW 320
                                                                                                                                                                                                                                                                                                                                                                                                                                       241
                                                                                                                                                                                                                                                                                                                                                                                                                                                        241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 LVPDCEHARMKVTTPCNSSGSLWDPNITVETLEAHOLRVSFTLWNESTHYQILLTSFPHM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        fvpdcedskmkmttscvssgslwdpnitvetldtqhlrvdftlwnestpyqvllesfsds 240
                                                                                                                                                                                                                                                                                                                                                                                                                      enhscfdvvkqifaprqeefhqranvtftlskfhwcchhhvqvqpffssclndclrhavt 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TNERLCVRFEELSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tnerlcvkfqflsmlqhhrkrwrfsfshfvvdpgqeyevtvhhlpkpipdgdpnhkskii 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                               Spriggs
                                                                                                  96US-0620694.
95US-0410535.
95US-0538765.
                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                     96US-0620694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                       /label= signal_peptide
32..864
                                                                                                                                                                                                             Location/Qualifiers
1..31
                                                                MK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71.18;
71.48;
                                                              27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1254; DB 19;
Pred. No. 6.7e-118;
30; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
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AAY99935
ID AAY9
XX AAY9
AC AAY9
XX IO-J
XX II-1
XX II
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                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 230; Conserv
                                                                                                                           Domain
                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                     Mus sp.
                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                       IL-17R; CTLA-8; interleukin 17; Herpesvirus saimiri; HVS
murine; antibody; immune suppression.
                                                                                                                                                                                                                                                                                                                                                                                          Murine IL-17R protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                   10-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY99935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY99935 standard; Protein; 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 VSCPEMPDT--PEPIPDYMPIW 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents a murine interleukin-17 receptor (IL-17R). IL-17R polypeptides have immunoregulatory activity. They can be used for particular they can be used for preventing T cell proliferation, or for inhibiting T cell activation. In rejection, autoimmune disease, allergy or astima. They can also be used for preventing or treating organ or graft activated T cells play a role or for inhibiting B cell proliferation or timmunoglobulin secretion. The IL-17 polypeptides can also be used or immunogens, reagents in in vitro assays, or as binding agents for affinity purification procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             asthma or inflammatory disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGAARSPPSAVPGPLIGLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vpcpvisnttvpkpvadyiplw 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   enhscfdvvkqifaprqeefhqranvtfflskfhwcchhhvqvqpffssclndclrhavt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               {\tt tnericv} kfqfls {\tt mlqhhrkrw} rfsfshfvvdpqqeyevtvhhlpkpipdqdpnhkskii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TNERLCVRFEFLSKLRHHHRRWRFTESHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWIHPRNITPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          swihpknltpsspkniyinlsvsstqhgelvpvlhvewtlqtdasilylegaelsvlqin
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                                                                      /label= 1
354..864
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                              /label= Cytoplasmic_domain
32..864
                                                                                                                      /label= Extracellular_domain 323..353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Column 25-30; 25pp; English.
                                                                                                                                                            /label= Signal_peptide 32..322
                                                                                                                                                                                                                 Location/Qualifiers
1..31
'label= IL-17R
                                                                                                                    353
                                                                           Transmembrane_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.18;
71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 1254; DB 20;
; Pred. No. 6.7e-118;
30; Mismatches 60;
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The present invention relates to a novel receptor that binds Interleukin CC (17 (IL-17, also known as CTLA-8) and a Herpesvirus saimiri homolog, CC (17 (IL-17, also known as CTLA-8) and a Herpesvirus saimiri homolog, CC (17 (IL-17, Murine thymona EL4 cells were found to express a CC to as IL-17R. Murine thymona EL4 cells were found to express a CC (12 (IL-17). An EL4 mammalian expression library was screened CC and a cDNA encoding the receptor was identified. The present sequence CC (18 (IL-17R) protein. The cDNA was used to isolate DNA encoding CC (18 (IL-17R) by cross species hybridisation. The human IL-17R cDNA and CC protein are described in AAA61240 and AAY9941. Soluble forms of the CC suppress rejection of organ grafts. Antibodies to IL-17R consisting of CC amino acids I-322 of murine IL-17R or 1-320 of human IL-17R may be useful CC as components of diagnostic or research assays. Such antibodies may also be used in affinity purification of the receptor.
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                                                                                                                                                                                                                                                                                                   Query Match 71.1%; Score 1254; DB 21; Best Local Similarity 71.4%; Pred. No. 6.7e-118; Matches 230; Conservative 30; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-1996;
23-MAR-1995;
07-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibodies immunoreactive with interleukin-17 receptor protein useful in interfering with receptor binding to CTLA-8, as components of diagnostic or research assays or in affinity purification of the receptor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US6072037-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Column 25-30; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-411206/35.
N-PSDB; AAA61238.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fanslow WC,
                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                 241
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                                                                                                                                                                                                                                                  864 AA;
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95US-0410535.
95US-0538765.
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Search completed: July 17, 2001, 11:18:55 Job time: 194 sec

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OM protein - protein search, using sw model
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                      SPTREMBL_16:*
1: sp_archea:*
2: sp_bacteria:
3: sp_fungi:*
4: sp_human:*
4: sp_human:*
5: sp_inverteb:
6: sp_manmal:*
7: sp_mhc:*
8: sp_organel1:
9: sp_plane:*
10: sp_plane:*
11: sp_rodent:
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1766
1 MAIRRCWPRVVPGPALGWLL......CPVISNTTVPKPVADYIPIW 322
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Gapop 10.0 , Gapext 0.5
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sp_rodent:*
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sp_human:*
sp_invertebrate:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	ω	2		Result
87.5	87.5	88	88	89.5	91	91.5	92	94.5	97.5	99.5	112.5	140.5	231	247.5	280.5	282.5	1254	1766	Score
5.0	5.0	5.0	5.0	5.1	5.2	5.2	5.2	5.4	5.5	5.6	6.4	8.0	13.1	14.0	15.9	16.0	71.0	100.0	Query Match Length
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82.5	82.5	82.5	82.5	82.5	83	83	83	83.5	83.5	83.5	83.5	84	84	84.5	84.5	84.5	85	85	85	85.5	85.5	85.5	86.5	86.5	87)
4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8	. 8	4.8	4.8	4.9	4.9	4.9	•
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ALIGNMENTS

DP 48	2	Db	Qy	Db	Ωу		SQ	ב אַכ	R R	RT	RT.	0 7	D RX	RC	RP.	D.	<u>۾</u> ۾	8	SO	GN E	ין בי דו דו	i Pi	DT	AC	E S	RES
121	131	61	61 SWIHDKNLTDSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120	H	1 MAIRRCWPRVVPGPALGWLLLLLINVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60	Query Match 100.0%; Score 1766; DB 11; Length 864; Best Local Similarity 100.0%; Pred. No. 5.9e-163; Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	SEQUENCE 864 AA; 97807 MW; 343FD51AA687DA31 CRC64;	MgD: Mg1:107399; I117r.	Immurity 3:811-821(1995).	novel cytokine receptor.";	"Herpesvirus Saimiri encodes a new cytokine, IL-17, which binds to a	.K.;	MEDLINE=90111900; FUNECTONIAN, Painter S.L.,	TISSUE-THYMOMA EL4;	SEQUENCE FROM N.A.		Mammalia; Euchelia; Nodencia, Sciuloguania;		sculus (Mouse).		5		01, Creat		ID 060943 PRELIMINARY; PRT; 864 AA.	RESULT 1

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RESULT
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Matches 230
               Q9NRL4;
Q9NRL4;
01-OCT-2000
01-OCT-2000
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receptor.";
Cytokine 9:794-800(1997).
Cytokine 9:794-800(1997).
CMBL; U58917; AAB99730.1; -
EMBL; U58917; AAB99730.1; -
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043844;
01-JUN-1998 (TrE
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01-NOV-1998 (TrE
IL-17 RECEPTOR.
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MEDLINE-98035683; PubMed=9367539;
Yao Z., Spriggs M.K., Derry J.M.J., Strockbine L.,
VandenBos T., Zappone J., Painter S.L., Armitage R.
"Molecular characterization of the human interleuki
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Primates; Catarrhini; Hominidae;
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                                                                            PRELIMINARY;
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Pred. No. 3.1e
30; Mismatches
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Last annotation updat
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Best Local Similarity
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MEDLINE=20273223; PubMed=10815801;
Tian E., Sawyer J.R., Largaespada
Shaughnessy J.D. Jr.;
"Evi27 encodes a novel membrane pr
receptor.";
Oncogene 19:2098-2109(2000).
EMBL; AF208110; AAF86051.1;
                                                                                                            EVI27.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; F
Catarrhini; Hominidae;
                                                                                                                                                                          QONRM6;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
IL-17 RECEPTOR HOMOLOG PRECURSOR.
                                                                                                                                                                                                                                                 Q9NRM6
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                            171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A novel cytokine receptor-ligand pair characterization, and in vivo immunomodu Biol. Chem. 275:19167-19176(2000). EMBL; AF212365; AAF78776.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20317118; PubMed=10749887;
Shi Y., Ullrich S.J., Zhang J., Connolly K., Grzegorzewski Barber M.C., Wang W., Wathen K., Hodge V., Fisher C.L., Ols Ruben S.M., Knyazev I., Cho Y.H., Kao V., Wilkinson K.A., Carrell J.A., Ebner R.;
                                                                                                                                                                                                                                                                                                            278
                                                                                                                                                                                                                                                                                                                                   313
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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IL-17B RECEPTOR.
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                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                 PubMed=10815801;
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Pred. No. 3e
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                                            protein
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                                                                 Jenkins N.A.,
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SQ FT WW

Signal; SIGNAL SEQUENCE CHAIN

Receptor 14 502

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POTENTIAL.
IL-17 RECEPTOR HOMOLOG.
9C84A63EC123FF17 CRC64;

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Best Local Similarity
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                                                             В
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Best Local Similarity
                                                                                                                                                                Matches
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE=20273223; PubMed=10815801;

Tian E., Sawyer J.R., Largaespada D.A., Jenkins N.A.,

Shaughnessy J.D. Jr.;

Shaughnessy J.D. Jr.;

Tevi27 encodes a novel membrane protein with homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVI27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9JIP3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194
                                                                                                                                                                                                                                                                                                                         Signal; Receptor.
                                                                                                                                                                                                                                                                                                                                                                      Oncogene 19:2098-2109(2000).
EMBL; AF208108; AAF86049.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          278
                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                     receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HRK----RWRFSFSHFVVDDGQEYEVTVHHLPKPIPDGDPNHKSKIIFVPDCEDSKMKMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPYTTSVATGDYSILMNVSWVLRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVL-QLNTNERLCVKFQFLSMLQH 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVLISLAALCRSAVPR---EPTVQCGSE-----TGPSPEWMLQHDLIPGDLRDLRV 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLLLNVLAPGR-ASPRLLDFPAPVCAQEGLSCRVKNSTCLDDSWIHPKNLTPSSPKNIYI 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APRQEEFHORANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVTVP-CPVISNTTVP 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KKCVKAGSLWDPNITACKKNEETVEVNFTTTPLGNRYMALIQ------HSTIIGFSQVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPHOKK-QTRASVVIPVTGDSEGA--TVQLTPYFFTCGSDCIRHKGTVVLCP---QTGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FPLDNNKSKPGGWLPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88;
                                                                                                            LLLLINVLAPG--RASPRLLDFPAPVCAQEGLSCRVKNSTCLDDSWIHPKNLTPSSPKNI
                                                                     ### HILVILILAASCRSALPR---EPTIQCGSE-----TGPSPEWMVQHTLTPGDLRDL
Conservative
                                                                                                                                                                                                                                                                                    499
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ilarity 25.4%;
Conservative 5
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499
55617 MW;
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27.8%;
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Pred. No. 5.7e-19;
1; Mismatches 138;
                                                                                                                                                                     50;
                                                                                                                                                                                                                                                                                                          POTENTIAL
IL-17 RECI
                                                                                                                                                                Score 247.5; DB 1
Pred. No. 9.1e-16;
0; Mismatches 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleosto
Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                    L-17 RECEPTOR HOMOLOG.
C66440430E3C31F3 CRC64;
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                                                                                                                                                                                                                      DB 11;
                                                                                                                                                                       140; Indels
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                                                                                                                                                                                                                    Length 499;
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Best Local S
Matches 79
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
TRUNCATED IL-17 RECEPTOR HOMOLOG PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9NRM5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9NRM5
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-20273223; PubMed-10815801; Tian E., Sawyer J.R., Largaespada Shaughnessy J.D. Jr.;
                                                                                                                                                                                                                                                                                                                                                                                  Oncogene 19:2098-2109(2000).
EMBL; AF208111; AAF86052.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136
                                                                                                                                                                                                                                                                                                                                                         Signal; Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                       "Eviž7 encodes a novel membrane protein with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 QVELVKTSVAAEEFSILMNISWILRADASIRLLKATKICVSGKNNMNSYSCVRCNYTEAF
                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                            receptor.
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                        224
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                                                                                                                                                                                                                                              20 LLLLNYLAPGR-ASPRLLDFPAPYCAQEGLSCRYKNSTCLDDSWIHPKNLTPSSPKNIYI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLE-----SFSDSENHSCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QHHRK----RWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKIIFVPDCEDSKMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVTVPCPVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RT--SVAIPVTEESEGAV-----
                                                                       KKCVKAGSLWDPNITACKKNEETVEVNFTTTPLGNRYMALIQ-----
                                                                                      TSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDSENHSCEDVVKQIF 253
                                                                                                                        QTRPSGGKWTFSYIGFPVELNTVYFIGAHNIPNANMNEDGPSMSVNFTSPGCLDHIMKYK 170
                                                                                                                                              HRK----RWRFSFSHFVVDDGQEYEVTVHHLPKPIPDGDPNHKSKIIFVPDCEDSKMKMT 193
                                                                                                                                                                      EPVTTSVATGDYSILMNVSWYLRADASIRLLKATKICVTGKSNEQSYSCVRCNYTEAFQT 110
                                                                                                                                                                                      NLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVL-QLNTNERLCVKFQFLSMLQH 137
                                                                                                                                                                                                                       LVLISLAALCRSAVPR---EPTVQCGSE-----TGPSPEWMLQHDLIPGDLRDLRV
  CLRHAVT
                        EPHQKK-QTRASVVIPVTGDSEGATVQVKFSELLWGGKGHRRLFHHSLLLR--MSSLLSN
                                                APRQEEFHQRANVTFTL---
                                                                                                                                                                                                                                                                        l Similarity
79; Conser
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288 AA;
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                                                                                                                                                                                                                                                                        Conservative
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288 T
31773 MW;
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                                                                                                                                                                                                                                                                            48;
                                                                                                                                                                                                                                                                          Score 231; DB 4; Length 288, pred. No. 1.9e-14; 18; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291
                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
TRUNCATED IL-17 RECEPTOR HOMOLOG
CD8EB2C0C235FBFB CRC64;
                                                    SKFHW----CCHHHVQVQPFFSSCLND 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          288
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                                                                                -HSTIIGFSQVF
                                                                                                                                                                                                                                                                                48;
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281 ALLPADT

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                      Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
    Harris D., Wood V., J
Submitted (FEB-2000)
                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PUTATIVE TRANSCRIPTIONAL ACTIVATOR.
                                                                                                                                                                   Q9Р7Н9;
Q9Р7Н9;
                          STRAIN-972H-;
                                                          Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                              SPAC105:03C
                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE=20273223; PubMed=10815801;
Tian E., Sawyer J.R., Largaespada D.A.,
Shaughnessy J.D. Jr.;
"Evi27 encodes a novel membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal; Receptor.
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9JIP2;
                                                                                                                                                                                                                                  :|:
169 VTS 171
                                                                                                                                                                                                                                                       192 MTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oncogene 19:2098-2109(2000).
EMBL; AF208109; AAF86050.1;
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01-OCT-2000
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                                                                                                                                                                                                                                                                  QSQTRPSGGKWTFSYVGFPVELSTLYLISAHNIPNANMNEDSPSLSVNFTSPGCTRENTE
                                                                                                                                                                                                                                                                                       QHHRK----RWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKIIFVPDCEDSKMK 191
                                                                                                                                                                                                                                                                                                            QVELVKTSVAAEEFSILMNISWILRADASIRLLKATKICVSGKNNMNSYSCVRCNYTEAF
                                                                                                                                                                                                                                                                                                                             YINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVL-QLNTNERLCVKFQFLSML
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                                                                                                                                                                                                                                                                                                                                                                         LLLLLNVLAPG--RASPRLLDFPAPVCAQEGLSCRVKNSTCLDDSWIHPKNLTPSSPKNI 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 RECEPTOR HOMOLOG
                                                                                                                                                                                                                                                                                                                                                                                                       1 Similarity
45; Conserv
                                                                                                                                                                                                                                                       194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         218 AA;
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218
23855 Þ
Rajandream M.A., Barrell B.G.; to the EMBL/GenBank/DDBJ databases
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24.6%;
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Last annotation update
TISOFORM PRECURSOR.
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Pred. No. 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
IL-17 RECEPTOR HOMOLOG SHORT
; E17C154C824E1F0B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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hes 87;
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P79927; PTEMBLIEL 03, Created)
01-MAY-1997 (TIEMBLIEL 03, Last seque
01-MAY-1997 (TIEMBLIEL 03, Last seque
01-MAR-2001 (TIEMBLIEL 16, Last annot
INTEGUMENTARY MUCIN B.1 (FRAGMENT).
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Best Local S
Matches 63
                                                                                                                                                                                                             NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                       InterPro: IPR000436; -.
InterPro: IPR001846; -.
InterPro: IPR001919; -.
Pfam: PF00084; sushi; 1.
Pfam: PF00094; vwd; 3.
Pfam: PF01826; TIL; 1.
                                                                                                                                                                                                                                                                                                                      Pfam;
                  495
                                                                                                                                                                                                                                                            SMART;
                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                             "Similarities of integumentary mucin B.1 from Xenopus laevis prepro-von Willebrand factor at their amino-terminal regions Piol. Chem. 272:1805-1810(1997).
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Y08296; CAA69604.1;
HSSP; P19398; LATB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97153143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; (Amphibia; Batrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Joba W., Hoffmann W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus laevis (African clawed frog).
                                                            56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL157994; CAB76236.1; -.
Interpro; IPR003015; -.
PROSITE; PS00038; HELIX LOOP_HELIX; UNKNOWN_1.
PROSITE 708 AA; 80989 MW; 78F57C5A0EB2DE76 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221 FDDSLSYAYILNPTSDSD----VDLIRQYFIPKEG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224
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TCNGGTWTCSKGSCPGICKVEEGVYVTTYDGITYSMHGNCVYIISMHTSWLVYAKLSQSQ
                                       TCLDDSWIHPKNLTPSSPK----NIYINL--SVSSTQHGELVPV--LHVEW------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----FVPDCEDSKMKMTT-----SCVSSGSLWDPNITV----ETLDTQHLRVDFTL 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --QFPSITQNEENFRFKKSFTQ---------PQPIVKETTFPKSEPGQEHAKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KFQFLSMLQHHRK-RWRFSFSHFVVDPGQEYEVTVHHLPKPI-----PDGDPNHKSKII 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQPNLCIPCSLGTCLIHFHEFSSSSFMDPVSLFCSSP---YPNLPPHSRSSSLESKKPSV
                                                                                                                                                                                                                                                         SM00032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASQDVKSDGTLPIGTNNNPLIPSHSQESSHWTIRHESMPSALAGSSAQSMQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SS------TQHGELVPVLHVE---WTLQTDASILYLEGAELSVLQLNTNERLCV
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                                                                                               Similarity 21.: 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63;
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                                                                                                                                                                                                           1506 AA;
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                                                                                                                                                                                                                             CCP; 1.
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                                                                                                                    5.6%;
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                                                                                                                                                                                                      163905 MW;
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                                                                                                  35;
                                                                                        Score 99.5; DE
Pred. No. 0.78;
35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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Pred. No. 0.018;
                                                                                                                                                                                                 7BF269A748DC817F CRC64;
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                                                                                                                                       DB
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                                                                                                                                Length
                                                                                           Indels
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                                                                                                                                  1506;
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
EXTERIOR MEMBRANE PROTEIN GP120 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Predominance of subtype A and G HIV type 1 in Nigeria, with geographical differences in their distribution.", AIDS Res. Hum. Retroviruses 16:315-325(2000).
EMBL; AJ389751; CAB77485.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=96NG-MACSW031;
MEDLINE-20179113; PubMed-10716369;
Peeters M., Esu-Williams E., Vergne L., Montavon
Mulanga-Kabeya C., Harry T., Ibironke A., Lesage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9IU91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000777; -. Pfam; PF00516; GP120; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENV
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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 290
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CLNDCLRHAVTVPCPV 305
                                                                                                                IFVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNE---STPYQV-LLE
                                                                                                                                                      ETIEINCTRPN----NNTRKSIRFG-----PGQAFYAT---
                                                                                                                                                                        -TNERLCYKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKI 179
                                                                                                                                                                                                                                                                              LINCNVSAINQACPKVSFDPIPIHYCAPAGFAILKCRDKNFNGTGTC----
                                                                                                                                                                                                                                                                                                           LLLLNVLAPGRASPRILDFPAPV--CAQEG---LSCRVKN----STCLDDSWIHPKNLTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LFANQQCSQLKDPNGAFAK-----CHSTVLYRSFYERCVHLTCISQDMTVSMCTELRN 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DAQSSTIINSVSLVLNLGNQESTYTFNRDGSIINEKMTNQNVFQSDQLSISRSGTFIIVL 614
                                                         SFS-----DSENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSS 289
                                                                                                                                                                                                                 -----KIVSTVQCTHG-IKPVVSTQLLLNGSLAEEDIVIRTENYTDNAKIIIVQLN 160
                                                                                                                                                                                                                                    SSPKNIYINLSVSSTQ--HGELVPVLHVEWTL----QTDASIL---YLEGAELSVLQLN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDSENHSCFDVVKQ 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THLHVNLLIQTGTTMQFYTSVPSTGYEDTEG-----PCGSFNHKADDDFM-----SNQK 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QHHRKRWRF----SFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKIIFVPDCEDSKMK 191
                              SFKNKNISFDSSSGGDLEITTHSFNCRGEFFYCNTSELFTKN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----TLQTDASILYLEGAELSVLQLN---
                                                                                                                                                                                                                                                                                                                                        h 5.5%;
Similarity 22.2%;
70; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                   328
328 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -PESSPETF-----VGF--WK----MSSCSDPVKPTCIDLEKE
                                                                                                                                                                                                                                                                                                                                                                                                                                    328
                                                                                                                                                                                                                                                                                                                                                                                                                    36504 MW;
                                                                                         -----IIENIRQAHCNVSRTKWNEMIQKVKVQLRKIE 223
                                                                                                                                                                                                                                                                                                                                           32;
                                                                                                                                                                                                                                                                                                                                        Score 97.5; DB Pred. No. 0.21; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    DE92C03A75CF898E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                328
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                                                                                                                                                                                                                                                                                                                                                                      DB 14;
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                                                                                                                                                                                                                                                                                                                                         85;
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٢: رو
                                                                                                                                                                                                                                                                                                                                                                    Length 328;
                                                                                                                                                                                                                                                                                                                                         Indels 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patrel D.,
                                                                                                                                                    -GD-----
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                              ST
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                              267
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RESULT 12
Q9FX72
ID Q9FX72
AC Q9FX72
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Best Local
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 Q9FX72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9JLN5 PRELIMINARY; PRT; 592 AA.
Q9JLN5;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
ERYTHROID MEMBRANE-ASSOCIATED PROTEIN ERMAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            membrane protein.";
Gene 242:337-345(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRALN=C57BL/6J;
MEDLINE=20184753; PubMed=10721728;
Ye T.-Z., Gordon C.T., Lai Y.-H.,
Perkins A.C., Chui D.H.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; 1g; 1. Pfam; PF00622; SPRY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR01407; BUTYPHLNCDUF PRODOm; PD000303; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF153906; AAF31162.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003596; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001870; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001211;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Ermap, a gene coding for a novel erythroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ERMAP
                                                                                527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    268 SKNST---TITLPCRI
                                                                                                                                                                                                                                                                                              303
                                                                                                                                                                                                                                                                                                                                                  263
                                                                                                                                                                                                                                                                                                                   125 LCVK--FQFLSMLQHHRKR------
                                                                                                                                                                                                                                          TAHPKLILSEDRRCVRLGDRKRPVPD-NPERFDFVVSVPGSE----YFTTGCHYWEVYVG
                                                                                                                                                                                                                                                                                                                                                                  PKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLNTNER
                                                                              IICTELQKSEESIVP
                                                                                                        ISNTTVPKPVADYIP 320
                                                                                                                                                                                                                                                                                           LLYEQAMEVESLLEDHAKEKGRLHKALKKLRSELKLKRAAANAGWRRARLHFVAVTLDPD 362
                                                                                                                                                                                                                                                                                                                                               PERGSLSSPA---VALSV-----VLPVL------GLLILLGIWLICKQKKSKEK 302
                                                                                                                                  VG----
                                                                                                                                                                                      EKTKWILGVCSESVSRKGKVTASPANGHWLVRQSRGNE - - - YEALTSPQTSFRLKESPKC
                                                                                                                                                                                                              SGSLWDPNITVETLDTQ------HLRVDFTLWNESTPYQVLLE---SFSDSENHSC
                                                                                                                                                                                                                                                                  QEYE-----VTVHHLPKPIPDGDPNHKSKIIFVPDCEDSKMKMTTSC-----VS
                                                                                                                                                          FDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVTVPCPV 305
                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
69; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SM00406; IGV;
CE 592 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR000107;
                                                                                                                                  - IFLDYEAGIISFYNVTDKSHIFTFTHSFSSPLRPFFEPCLHDEGKNT----APL
                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66555 MW;
                                                                                                                                                                                                                                                                                                                                                                                                               5.4%;
                                                                                541
                                                                                                                                                                                                                                                                                                                                                                                                   39;
                                                                                                                                                                                                                                                                                                                                                                                                   Score 94.5; DE Pred. No. 0.8; 39; Mismatches
                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    246AC691B8788BE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fujiwara Y.,
                682
                                                                                                                                                                                                                                                                                                                      -----WRFSFSHFV---VDPG 154
                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                    112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        specific
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                                                                                                                                                                                                                                                                                                                                                                                                                             Length 592;
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                                                                                                                                                                                                                                                                                                                                                                                                    95;
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                                                                                                                                                                                                                                        417
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                                                                                                                                   526
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Purnelle B., Goffeau A
Barrell B.G.;
Submitted (FEB-1998) t
EMBL; AL021767; CAA169
                                                                                                                                                                                                01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 06, Last annotation updat
                                                                                                                                      Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetales;
                                                                                                                                                                                        VACUOLAR PROTEIN SORTING-ASSOCIATED SPBC16C6.02C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pederspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F., Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks Buehler E., Chao Q., Chin C., Chiou J., Choi E., Gonzalez A., Howng B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M., Lenz C., Liu A., Liu S., Mukharsky N., Pham P., Sakano H., Shin Toriumi M., Vaysberg M., Wukharsky N., Theologis A., Davis R Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                          Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                    042926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last seq
01-MAR-2001 (TrEMBLrel. 16, Last ann
                                                             STRAIN=972H-;
                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F19K19.13 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102 TDASIL-YLEG---AELSVLQLNTNERLC------VKFQFLSMLQHHRKR 141
                                                                                                                                                                                                                                                                                                                                                                                              286 FFSSCLNDCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 KNLTPS-----SPKNIYINLSVSSTQHGE--LVPVLHVEWTLQ-------
                                                                                                                                                                                                                                                                                                                                                                 YSSSTSKDCL
                                                                                                                                                                                                                                                                                                                                                                                                                             SRCEDKLHIRIKSDSYNPRNDEFDSHANILENRNEETRINRWFTNAIGRQC-----KLLR 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSCFD-----VVKQIFAPRQEEFHQRANVT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VIRWPLC-RTGLLHDREWMVQGLTGE-----ILTQKKVPEMSLIKTFIDLEEGLLSVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSD-----SEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDFIISSFASPPKKTGNGTVVSGRFPQ-LPSEDLESKESFPSHYLKSITVYPIKSCAGFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WRFSFSHFVVDPGQEYEVTV--HHLPKPIPDGD-----PNHKSKIIFV---PDCEDSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDGSWFGYLEVEKLASLSGIQLRAG-HICWDDNDVINGKPTGAVRVSFGYMSTFEDAKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KSLTPSAIWMHTTSLSIYVKKKLQALRHGNGAAVCVLYGSENLELSSHKSGPTVTFNLKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     682 AA;
                                                                                                                                                                                                                                                                                     PRELIMINARY;
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 CAA16910.1;
                                                                                                                                                                                                                                                                                                                                                                 564
                                                                                                                                                                                                                                                                                                                                                                                              295
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22.9%;
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77036 MW; D5713DF18EA87D94 CRC64;
                                              Α.,
                 to the EMBL/GenBank/DDBJ databases
                                             Wood V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36;
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 92; DB Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 109;
                                              Lyne
                                                                                                                                                                                                                                                                                    3131
                                              M., Rajandream M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10;
                                                                                                                                                                                                                     update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         FTLSKFHWCCHHHVQVQP
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                                                                                                                                                                                                              Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Coolson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Liaister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
                                                                                    Watson A., Weinstock L., Wilaliac
"2.2 Mb of contiguous nucleotide
elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O62453;
01-AUG-1998 (TrEMBLrel.
01-AUG-1998 (TrEMBLrel.
01-JAN-1999 (TrEMBLrel.
EMBL; AL021489; CAA16370.1; SEQUENCE 333 AA; 38801 M
                                                                                                                         Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.; "2.2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhabditidae; Pel
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans
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Y44A6C.2.
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                                                                       Nature 368:32-38(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2189 KFCLTKSVTFTPR-FVFKNHLDCTVSLREF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2133 DESGRKNRAMISIDNGTSWSADIGFDTLGSSS-QVEVRKTNES---DVCLLGMSISESSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2015 ILHTDSKSFLLMGINVPDLDLQPVDLPIIYTPISSGQDVQTSALLTASDKQDVVKLILKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245 CFDVVKQI-FAPRQEEFHQRANVTFTLSKF 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 IHPKNLTPSSPKNIY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EKLPGTNYVSK--VMIYPPYVIFNHTDLSIQVTSSSPNSIRYTIPSGSYSNDIKPYFYSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTV-----HHLPKPIPDGDPNHKSKIIFVPD 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLHV-----EWILQ-TDASILYL---EGAELSVLQLNINE------RICVKF 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VFARNLMDGSLQNDYPFLQLNILPTLQIENLLPYEINLRIIERSSGNDWRSSLSPGDSLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GYVPLDLACLYPLRIRPVSKLGFLWSNQIVDWHSLNKSPL---QYLTCESTSTSWKHNLL 1954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GWLLLLLNVLAPGRASP------RLLDF----PAPVCAQEGLSCRVKNSTCLDDSW 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (JAN-1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nematoda; Chromadorea; Rhabditida; Rhabditoidea; rinae; Caenorhabditis.
         38801 MW;
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07,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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Pred. No. 11;
         8B6CC20CE156DFBC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         333
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         CRC64
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                                                                                                                                                                                                                                                                                                                                                                                                      Coulson A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92
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Query Match Best Local Similarity

5.2%;

Score 91; Pred. No.

DB 5; 0.89;

Length 333;

Conservative

44;

Mismatches

Indels

84;

13;

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Q22531
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Best Local Similarity 21.2
Matches 65; Conservative
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Q22531;
1594 EMTKFLDLTLYLVNEDSLAPWEQAIEFFTEMLNR--FQYQPEIDTVRNYVIQITKN---A 1648
                                                                    1534 LPTGYRVDNAGSTSFARINYDDKSWYSIQAQLLSNMNTMSSTTRAMLLDDANFFYQSGRW 1593
                                                                                                                                                                                                                  1380 PGVAKPVISDTPPVFGIEPYYKGSALLNLLNNVLTPAVFQEGLS------SYLTQ 1428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thomas K.; Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases EMBL; Z30317; CAA82971.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
T16G12.1 PROTEIN.
                                                                                                                                             1489 Q--ANQQSCMSDETL------WNVPLFTQTPGALDFNWFVNFTGGNDATWL----RP 1533
                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001930; -.
Pfam: PF01433; Peptidase_M1; 3.
PRINTS; PR00756; ALADITASE.
PROSITE: PS00079; WILTICOPPER_OXIDASE1; UNKNOWN_1.
PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_2.
SEQUENCE 1815 AA; 207455 MW; 73EF51E9CA0359E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=6239;
                   215 QHLR-VDFTLW--NEST--PYQVLLESFSDSENHSCFDVVKQIFAPRQEEFHQRANVTFT 269 : : : | | | : | | : | | : | | : | | | | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [nterPro; IPR001117; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000130; -.
                                                                                                                                                                               118 QLNTNERLCVKFQFLSMLQHHRKRWR------FSFSHFVVDPGQEYEVTVHHLPKP 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248 VVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAV 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        210 RLQILSIQGNSWQNYWDPSDVLEGLNAE------LWNQTERNQ---HYFLNAEHRKNFK, 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               260 KIADHFYPDQED------GFGAELEHGVDLSEAFDFLKNDGTRVSV 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155 KMFQLD----YLSVTHSDWMVPSDLEEMENKIVYLDKSDFYDSDMNQFLRELKSGSSHS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 SHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKIIFV--PDCEDSKMKMTTSCVSSGS----
                                                                                                                                                                                                                                                                                                                   CRVKNSTCLD------DSWIHP----KNLTPSSPKNIYINLSVSSTQHGELVPVLHV
                                                                                                       IPDG------DPNHKSKIIFVPDCE-DSKMKMTTSCVSSGSLWDPNITVETLDT 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -------LWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDSENHSCFD 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ETAIPKTCDVLIIQNYVPAEMDRYQESVD-----QFMEKCHIREGVVLHH-EVYTNSP 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EWTLQTDASILYLEG---AELSVLQLNTNERLCVKFQFL-----SMLQHHRKRWRFSF 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDVSENTSLDYRSNHQQLLKSWISSTEKIAQLFPTTLRTFQVTPPM-----IAAILDL 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                    5.1%; Score 89.5;
21.2%; Pred. No. 9;
                                                                                                                                                                                                                                                                                                                                                                     44; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                       DB 5; Length 1815;
                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                   89;
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Qy 270 LSKFHW 275
:||| |
Db 1649 VSKFQW 1654
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Search completed: July 17, 2001, 11:20:41 Job time: 160 sec

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 17, 2001, 11:18:26; Search time 16.71 Seconds (without alignments) 660.100 Million cell updates/sec Perfect score: 1766
Sequence: 1766
Sequence: 1 MAIRRCWPRVVPGPALGWLL.......CPVISNTTVPKPVADYIPLW 322
Scoring table: BLOSUM62 Gapop 10.0, Gapext 0.5
Searched: 93435 seqs, 34255486 residues
Total number of hits satisfying chosen parameters: 93435
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Minimum DB seq length: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB -	ID	(
ב	101	5.7	880	ן	TYO3_RAT	P55146 rattus norv
2	99		449	Ľ	GAD_MOUSE	3 mus mus
ω	98	5.5	1748	1	YNR2_YEAST	0
4	97		880	٢	TYO3_MOUSE	43-
5	95		449	_	GAD_RAT	ratt
6	94	5.3	388	Н	GMCR_MOUSE	
7	9.		606	Н	PF20_CHLRE	chl
œ	88.5	٠	954	ب	YB79_YEAST	
9	87	٠	452	Н	GAD_HUMAN	
10	87	4.9	520	-ب		homo
11	8	4.9	2515	_	TUD_DROME	_
12	86.5		377	سا	ICE4_HUMAN	
13	œ	4.9	2569	سا	LMA3_MOUSE	
14	85.5	4.8	1164	L	DP3A_VIBCH	vibr
15	85	4.8	925	Н	DBL_HUMAN	
16	84.5	4.8	429	ب	EPC_RAT	
17	84.5	4.8	455	L	ZPR1_CAEEL	
18	83.5	4.7	1213	<u>, , , , , , , , , , , , , , , , , , , </u>	T2D2_DROME	
19	83	4.7	432	Н	BRAC_XENLA	
20	83	4.7	672	۲	KPCA_HUMAN	homo sap
21	83	4.7	672	Н	KPCA_RABIT	_
22		4.7	672	۲	KPCA_RAT	rattu
23		4.7	1038	ب	ITA4_HUMAN	
24		4.7	329	<u> </u>	GCC_RAT	rattu
25	82	4.6	672	ب	KPCA_BOVIN	9 bos ta
26	82	4.6	808	<u>_</u>	POLG_HPAVG	hepa
27	82		852	Н	POLG_HPAVC	hepat
28	81.5	4.6	1134	Н	IF3X_HUMAN	
29	81.5	4.6	1152	Н	ITAM_HUMAN	5 homo
30	81	4.6	510	ட	VL1_HPV22	human
31	81	4.6	672	<u>, </u>	KPCA_MOUSE	
3 2	81	4.6	839	_	POLG_HPAVT	8 simi
ω ω	80.5	4.6	421	L	EPC_MOUSE	-

45	44	43	42	41	40	39	38	37	36	35	34
78.5	78.5	79	79	79	79	79	79.5	79.5	79.5	80	80.5
4.4	4.4	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.6
450	377	3712	3418	887	745	488	716	658	392	666	2347
Н	1	1	ш	۳	ب	Н	۳	ب	ب	μ	ب
COPP_MOUSE	ICED_HUMAN	LMA_DROME	BRC2_HUMAN	MCM2_DROME	ZP2_MACRA	PHR_SYNY3	ZP2_PIG	KPC1_LYTPI	BM15_HUMAN	ZP2_RABIT	KROS_HUMAN
_								Q25378 ly			P08922 ho
mus musculu	mo sapien	osophila	mo sapien	osophila	caca radi	nechocyst	s scrofa	lytechinus	omo sapien	yctolagus	homo sapien

ALIGNMENTS

DR D	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	RESULT TYO3_R TYO3_R AC P AC P DT O DT O DT O O O T O O O O O O O O O
EMBL; D37880; BAA07119.1; HSSP; P11362; 1EGI. InterPro; IPR000719; InterPro; IPR001777; InterPro; IPR001777; InterPro; IPR00106; Pfam; PF00041; fn3; 2. Pfam; PF00047; ig; 2. Pfam; PF00069; pkinase; 1. PROSITE; PS00107; PROTEIN_KINASE_TYR; 1. PROSITE; PS00109; PROTEIN_KINASE_TYR; 1. PROSITE; PS00101; PROTEIN_KINASE_TOM; 1. Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding; Transferase; Phosphorylation; Transmembrane; Signal; Repeat;	SEQUENCE FROM N.A. TISSUE-Brain; MEDLINE-96104999; PubMed-7490270; Ohashi K., Honda S., Ichinomiya N., Nakamura T., Mizuno K.; Ohashi K., Honda S., Ichinomiya N., Nakamura T., Mizuno K.; "Molecular cloning and in situ localization in the brain of rat sky receptor tyrosine kinase."; J. Biochem. 117:1267-1275(1995)I. THE CENTRAL NERVOUS SYSTEMI. TUNCTION: MAY BE INVOLVED IN CELL ADHESION PROCESSES, PARTICULARLY IN THE CENTRAL NERVOUS SYSTEMI. TUNCTION: MAY BE INVOLVED IN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATEI. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEINI. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEINI. TISSUE SPECIFICITY: ABUNDANT IN THE BRAIN AND LOWER LEVELS IN OTHER TISSUESI. SIMILARITY: CONTAINS 70 THE TYR FAMILY OF PROTEIN KINASES. AXL/UFO SUBFAMILYI. SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE C2-TYPE DOMAINSI. SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINSI.	TY 1

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MOD_RES
SEQUENCE
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CARBOHYD
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   Eukaryota;
                    Mus musculus
                                   GABRD
                                                  RECEPTOR).
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                                                                                                                                                                                                                                  dWVP
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                                                                                                                                                                                                                                                                                                  EALAVV---
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78; Conserv
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   Metazoa;
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(Rel. 19, Last sequence u.)
(Rel. 38, Last annotation
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                    (Mouse)
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1 880
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     Chordata;
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                                                                   RECEPTOR
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BY SIMILARITY.
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BY SIMILARITY.
VALUE (GLCNAC.
N-LINKED 
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Pred. No. 0.75
53; Mismatches
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CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
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ATP (BY SIMILARITY).
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TYROSINE-PROTEIN KINASE RECEPTOR TYRO3.
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     Craniata;
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                                                                   DELTA
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No. 0.
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ion update)
ELTA SUBUNIT
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YLATION (AUTO-) (BY SIMILA
86AAE5FA5B CRC64;
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      Vertebrata;
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                                                                   PRECURSOR (GABA(A)
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(POTENTIAL).
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      Euteleostomi;
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Query Match
Best Local S
Matches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the murine GABA, receptor.";
Brain Res. Bull. 29:119-123(1992).

Brain Res. Bull. 29:119-123(1992).

-I-FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN TOURCE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING CONTROL OF THE MAJOR AND OPENING AN INTEGRAL CHLOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sommer B., Poustka A., Spurr N.K., Seebur "The murine GABAA receptor delta-subunit assignment to human chromosome 1."; DNA (Cell Biol. 9:561-568(1990).
                                                  CARBOHYD
DISULFID
CONFLICT
SEQUENCE
                                                                                                                           TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                             EMBL;
EMBL;
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                     modified and this statement is not removed. entities requires a license agreement (See
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-91103876; PubMed=2176788; Spurr N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                           or send an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=DBA/2J; TISSUE-Brain;
MEDLINE=92370453; PubMed=1324097;
Wang J.B., Kofuji P., Burt D.R.;
"Strain comparisons and developmental
                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                          EMBL;
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                                                                                                                                                           DOMAIN
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                                                                                                                 DOMAIN
                                                                                                                                                                                                               Postsynaptic membrane;
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                                                                                                                                                                                                     ransmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHANNEL.
SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO. SUBCELLULAR IOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EN
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M60588;
M60589;
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M60595;
M60595;
S42882;
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            Similarity
                                                                                                                                                                                                                        PS00236;
                                                                                                                                                                                                                                                                                                                                                                                                                           equires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
                                                 164
255
449
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AAA37652.1;
AAA37652.1;
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AAA37652.1;
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rane; Ionic channel; Glycoprotein; Signal;
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            5.6%;
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  Score 99; DB
Pred. No. 0.48
44; Mismatches
                                                     BY SIMILARITY.
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                                                                                  N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
                                                                                                       CYTOPLASMIC PROBABLE.
                                                                                                                             PROBABLE
                                                                                                                                      PROBABLE
                                                                                                                                                  PROBABLE.
                                                                                                                                                            EXTRACELLULAR
                                                                                                                                                                       SUBUNIT
                                                                                                                                                                                GAMMA-AMINOBUTYRIC-ACID RECEPTOR DELTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seeburg P.H.;
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                       DB 1;
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             .48;
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                        Length 449;
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Conservative

44;

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Indels

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Gaps

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RESULT 3
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P53886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z71448; CAA96060.1; -. SGD; S0005116; YNL172W. Hypothetical protein; TransmuTRANSMEM 1378 1398 SEQUENCE 1748 AA; 196142 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Obermaier B., Piravandi E., Rinke M., Domdey H.; Submitted (MAY-1996) to the EMBL/GenBank/DDBJ datab-i- SIMILARITY: TO A.NIDULANS BIME AND MOUSE TSG24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
HYPOTHETICAL 196.1 KDA PROTEIN IN RPS3-PSD1 INTERGENIC REGION.
YNL172W OR N1677.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomycetales; NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118
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                                                                                                                                                                                                                                                                                                                                                        29 GRASPRLLDFPAP-VCAQEGLSC---RVKNSTCLDDSWIHPKNLTPSSPKNIYINLSVSS
                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 69; Conserv
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                                                                                                                                                                                                       TQHGELVPV-----LHVEWTLQTDASILYLEGAELSVLQLN-----TNERL----CVKFQ 130
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                                                                                                                                                                                                                                                                                          GNASGRTDIFALPSSCSRRSLSATLDRMGNN-----IAPTN--RAAPSGFFDSSSANT 339
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fw; 34BC9212020BB2B5 CRC64;
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-MTTSC---VSSGS----
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   LWDPNITVETLDT
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SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-Brain;
STRAIN-BALB/C; TISSUE-Brain;
STRAIN-BALB/C; TISSUE-Brain;
MEDLINE-95240399; PubMed-7722626;
MEDLINE-95240399; PubMed-7722626;
Schulz N., Paulhiac C., Lee L., Zhou R.;
Schulz N., Paulhiac C., Lee L., Zhou R.;
TISOLation and expression analysis of tyro3, a murine growth factor receptor tyrosine kinase preferentially expressed in adult brain.";
Teceptor tyrosine kinase preferentially expressed in adult brain.";
Teceptor tyrosine kinase preferentially expressed in adult brain.";
Teceptor tyrosine kinase preferentially expressed in adult brain.";
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P55144;

p55144;

p1-OCT-1996 (Rel. 34, Created)

01-OCT-1996 (Rel. 34, Last sequence update)

01-OCT-2000 (Rel. 40, Last annotation update)

TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (EC 2.7.1.112)

TYROSINE-PROTEIN KINASE RSE) (TYROSINE-PROTEIN KINASE DTK) (TK19-2).
                                                                              Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
-- FUNCTION: MAY BE INVOLVED IN CELL ADHESION PROCESSES,
-- IN THE CENTRAL NERVOUS SYSTEM.
-- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + I
TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-95161079; PubMed-7857657;
Crosier P.S., Lewis P.M., Hall L.R.,
Beier D.R., Wood C.R., Crosier K.E.;
                                                                                                                                                                                SEQUENCE FROM I
STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                 "Structure, expression, and activity of Tyro related receptor tyrosine kinase."; Oncogene 9:2567-2578(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6;
MEDLINE=94336210; PubMed=8058320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cells:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mark M.R., Scadden D.T., Wang 2., Gu Q., God "RSE, a novel receptor-type tyrosine kinase is expressed at high levels in the brain."; J. Biol. Chem. 269:10720-10728(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYRO3 OR DTK OR RSE
                                                                                                                                                                  Sasaki M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Growth
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                     Lai C., Gore M., Lemke G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Isolation of a receptor tyrosine kinase (DTK) from embryonic s cells: structure, genetic mapping and analysis of expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN TISSUE SPECIFICITY: ABUNDANT IN THE BRAIN AND
               OTHER TISSUES.
SIMILARITY: BELONGS
   AXL/UFO SUBFAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       structure, genetic mapping and Factors 11:125-136(1994).
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                   TYR FAMILY OF PROTEIN KINASES
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PROSITE; PS00107; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50011; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
DOMAIN
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Pfam; PF00041; fn3; 2.

Pfam; PF00047; 1g; 2.

Pfam; PF00069; pktnase; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
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InterPro; IPR001245; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
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 111
                       55
                                           51
                                                                 \vdash
                                                                                    1 MAIRRC--WPRVVPGPALGWLLL--LLNVLAPGRASP--RLLDFPAPVCAQEG----LSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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; U18933; AAC52148.1;
; X78103; CAA54995.1; I
; U18342; AAB26942.1; I
 GAELSVLQLNTNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDP--
                       SVEGMEDPDIHWMKDGTVVQNASQ-----VSISISEH-SWIGLLSLKSVERSDAGLYWCQ
                                         RVKNSTCLDDSWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLE
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77; Conser
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AAB26942.1; ALT_INIT.
                                                                                                                                                               AA;
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21.0%;
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2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                LLLAGLASLLLPGSAAAGLKLMGAPVKMTVSQGQPVKLNC
                                                                                                          55;
                                                                                                         Score 97; DB 1
Pred. No. 1.6;
55; Mismatches
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N-LINKED
N-LINKED
N-LINKED
N-LINKED
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A -> R (IN REF. 3).
L -> V (IN REF. 3).
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IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
FIBRONECTIN TYPE-III.
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TYROSINE-PROTEIN KINASE RECEPTOR
EXTRACELLULAR (POTENTIAL).
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                     the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                      This
                                                                                                                                                                                                                                                                                                  MEDLINE=90179746; PubMed=1690000;
Zhao Z.Y., Joho R.H.;
"Isolation of distantly related members in a multigene
the polymerase chain reaction technique.";
Biochem. Biophys. Res. Commun. 167:174-182(1990).
                                                                                                                                                                                                                                                                                                                                                                                                               subpopulations.";
Neuron 3:327-337(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                          Shivers B.D., Killisch I., S
Schofield P.R., Seeburg P.H.
"Two novel GABAA receptor su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GABRD
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90380375; PubMed=2561970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
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                                                                                                                                  CHANNEL.
SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
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                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
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SEQUENCE
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01-OCT-2000 (Rel. 40, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR
                                                                SEQUENCE FROM N.A.
TISSUE-Neonatal spleen;
MEDLINE-92263426; PubMed-1533931;
Park L.S., Martin U., Sorensen R.,
                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                        CHAIN PRECURSOR (GM-CSF-R-ALPHA) (GMR). CSF2RA OR CSFGMRA.
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InterPro; IPR001175; -.
Pfam; PF00065; neur_chan;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M35162; AAA41182.1; PIR; JQ0076; JQ0076. PIR; A34625; A34625.
"Cloning of the low-affinity murine granulocyte-macrophage colony-stimulating factor receptor and reconstitution of a high-affinity
                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                       GMCR_MOUSE
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                                                 Larsen A.;
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Pred. No. 1;
44; Mismatches
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EXTRACELLULAR
PROBABLE.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                     Craniata; Vertebrata;
Sciurognathi; Muridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROBABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAMMA-AMINOBUTYRIC-ACID RECEPTOR DELTA
                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64BDBCDEEB2C70AF CRC64;
                                                                   Luhr
                                                                                                                                                                                                                                                                                                                                                                                                     388
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                                                              s.,
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                                                                                                                                                                                          Muridae;
                                                                Morrissey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 449
                                                                                                                                                                                                                                                                                               RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                       Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal;
                                                              P.J.,
                                                                                                                                                                                                                                                                                                 ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92;
                                                                   Cosman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor complex.";
Proc. Natl. Acad. Sci. U.S.A. 89:4295-4299(1992).
-!- FUNCTION: RECEPTOR FOR GRANULOCYTE-MACROPHAGE COLONY-STIMULATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA CHAIN IS COMMON TO THE IL-5, IL-5 AND GM-CSF RECEPTORS (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
-i- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
                                        348
                                                                                                                                                                                                         187
                                                                                             301
                                                                                                                        181
                                                                                                                                                                                                                                                             135 CETRAARFLSCAW----REGPAAPADVRYSLRVLNSTGHDVARCMADPGDDV----ITQC
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                                         VTCRRFEVTRRLFPP
                                                                  ENHSCFDVVKQIFAP
                                                                                                                       FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS
                                                                                                                                                                                                                                 LQTDASILYLEGAELSVLQLNTNERLCVKF-----QFLSML------
                                                                                                                                                                                                                                                                              CRVKNSTCLDDSWIHPKNLTPSSPKNIYINLSV-SSTQH------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGI:1339754; Csf2ra.
                                                                                             ---RAGDTRMK-----HWGEWSPAHPLEAEDT---RVPGALLYAVTACAVLLCALALG
                                                                                                                                                  SWAPPSTWASLTARDFQFEVQWQSAEPGSTPRKVLVVEETRLAFPSPAPHG--GHKVKV-
                                                                                                                                                                              RW------RESFSHFVVDPGQE-----YEVTVHHLPKPIPDGDPNHKSKII 180
                                                                                                                                                                                                         IANDLSLL---GSEAYLVVTGRSGAGPVRFLDDVVATKALERLGPPRDVTASCNSSHCTV
                                                                                                                                                                                                                                                                                                                     RCWFRRMMALHHGVTLDVNGTVGGAAAHWRLSFVNESAAGSGA
                                                                                                                                                                                                                                                                                                                                               RCWPR------VVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLS
                                                                                                                                                                                                                                                                                                                                                                         l Similarity
68; Conserv
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1 29 POTENTIAL.
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N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                         Score 94; DB 1
Pred. No. 1.1;
35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR RECEPTOR ALPHA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
8C72E474360770FE CRC
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                                                                                                                                                                                                                                                                                                                                                                          108;
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(POTENTIAL).
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PF20_CHLRE ID PF20_C AC P93107

PF20_CHLRE P93107;

STANDARD;

PRT;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smith E., Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
FLAGELLAR WD-REPEAT PROTEIN PF20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00320; GPROTEINBRFT.
PROSITE; PS500878; WD_REPEARS_2; 6.
PROSITE; PS50082; WD_REPEARS_2; 6.
PROSITE; PS50294; WD_REPEARS_REGION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001680; -. Pfam; PF00400; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smith E., Lefebyre P.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
Submitted: INTER-MICROTUBULE BRIDGES IN FLAGELLA.
-I- SIMULARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
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                                                                                                   551 LA 552
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606 AA;
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Pred. No. 4.4;
34; Mismatches
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No: 4.
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GAD_HUMAN
ID GAD_H
AC 01476
DT 15-JU
DT 15-JU
DT 01-OC
DE GAMMA
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             15-JUL-1998
15-JUL-1998
01-OCT-2000
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1994 (Rel. 30,
01-OCT-1994 (Rel. 30,
15-JUL-1999 (Rel. 38,
PUTATIVE FAMILY 31 GLU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YB79_YEAST
P38138;
                                                      GAD_HUMAN
014764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dubois E., el Bakkoury M., Glansdorff N., Messenguy F., Pler Scherens B., Vierendeels F.; Scherens B., Vierendeels F.; Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. The European Bioinformatics Institute. The by non-profit institutions as long
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 GAMMA - AMINOBUTYRIC - ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; $46105; $46105.
SGD; $0000433; YBR229C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                           LGWLLLLLNYLAPGRASPRLLDFPAPYCAQEGLSCRYKNSTCLDDSWIHPKNLTPSSPKN
                                                                                                                                          ALKLIVNEQNFLNIEHH-----RTKQENF---AHVLPEETTFNMFKDNFLYSKH
                                                                                                                                                                                                FLKQKQTVN--
                                                                                                                                                                                                                         DSKMKMTTSCVSSGSLWDP----NITVETLDTQHLR---VDFTLWNESTPYQVLL----
                                                                                                                                                                                                                                                     LQDHSVRFTINEKERMPTNSSGLLISSQRFNETWKYAFDKKFQE-EANRTS----IPQFH 150
                                                                                                                                                                                                                                                                                 LQHH-----RKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKIIFVPDCE
                                                                                                                                                                   -----ESFSDSENHSCFDVVKQIFAPRQEEFHQRANV----TFTLSKFHWCCHHH
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             (Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 40, Last annotation updat
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38, Last annotation update)
GLUCOSIDASE IN FAT2-PBP2 INTERGENIC
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RECEPTOR DELTA SUBUNIT
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    PRECURSOR (GABA(A)
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Best Local
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DISULFID
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Day T.M., Hartnett C., Blankenbiller K., Ramabhadran T.V.; Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
-!- EUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO TGABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0252; NRIONCHANNEL.
PRINTS; PRO0253; GABAARECEPTR.
PROSITE; PS00238; NEUROTR_ION_CHANNEL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM;
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HOMO sapiens (Human).

Homo sapiens (Human).

""" Metazoa; Chordata;

""" harvota; Metazoa; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000188; -.
InterPro; IPR001175; -.
Pfam; PF00065; neur_chan;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entitles requires a license agreement (Some send an email to license@isb-sib.ch).
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT:
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CFDVVKQIFAPRQEEFH----
                                                                                        CEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDSENHS
                                                                                                                                                          KFQFLSMLQHHRKRWFSFSHFVVDPGQE--YEVTVHH-LPKPIPDGDPNHKSKIIFVPD
                                                                                                                                                                                                                           GIGGPPVNVALALEVASIDH----ISEANMEYTMTV---FLHQSWRDSRLSYNHTNETLGL
                                                                                                                                                                                                                                                                   ---SSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLNTNERLCV 127
                                                                                                                                                                                                                                                                                                                     APARLLAPLLL-----LCAQQLRGTRAMNDIGDYVGSNLEISWLPNLDGLIAGYARNFRP
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249
275
309
332
430
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103
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22.18;
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                                             -DMDLAKYPMDEQECMLD----
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-QRANVTFTLSKFHW
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 87;
Pred. No.
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GAMMA-AMINOBUTYRIC-ACID RECEPTOR DELTA SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      channel; Glycoprotein;
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BY SIMILARITY.
B4696518D39644C4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THERE ARE FIVE TYPES OF GABA(A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                              83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 452;
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; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                              84;
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IDC CPF2_HUMAN
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IDC
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
CYTOCHROME P450 4F2 (EC 1.14.13.30) (CYPIVF2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            HepG2
Arch.
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"Expression and molecular cloning 
hydroxylase (CYP4F2) gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hydroxylase gene HepG2 cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhang X., Chen L., Hardwick J.P.;
"Promoter activity and regulation of the CYP4F2 leukotriene hydroxylase gene by peroxisomal proliferators and retinoic and processing the control of the CYP4F2 leukotriene and retinoic and control of the CYP4F2 leukotriene and control of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Liver;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYP4F2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=10860554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-175 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lamerdin J.E., McCready P.M., Skowronski E., Adamson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Cell Biol. 18:723-730(1999).
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MONOXYGENASES. IN LIVER MICROSOMES, THIS ENZYME IS INVOLVED IN MADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. IT OXIDIZES A VARIET OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FAITY ACIDS, AND XENOBIOTICS.

CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH + OXIDIZED FLAVOPROTEIN + H(2)O.

SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
TISSUE SPECIFICITY: LIVER.

SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                  h. Biochem. Biophys. 378:364-376(2000). FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEDIV-YYWSESQEHIHGLDKLQLAQ--FTITSYHF 221
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se E., Kondo T.,
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Amico-Keller G.,
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AB015302;
AB015303;
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                                      HSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVTVP
                                                                                                       QRFRRACRLVHDFTDAVIQERRRTLPSQGVDDFLQAKAKSKTLDFIDVLLLSKDEDGK--
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U02388; AAC50052.1;
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W -> G (IN REF. 3).

WP -> CD (IN REF. 2).

WP -> CR (IN REF. 5).

GLSWVLYHLAKHPEYQER -> VSPGSCTTLQSTQNTRSV
                                                                                                                                                                                                                                                                                                            V -> M (IN REF. 3).
R -> A (IN REF. 2).
KPELVLRAEGGLWLRVE ->
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LH -> CI (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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01-MAY-1992 (Rel. 22,
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MATERNAL TUDOR PROTEIN
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Pfam; PF00567; TUDOR; 10.
Developmental protein.
SEQUENCE 2515 AA; 285236 MW;
                                                                                                                                                                                                                                                                                                                                                                                      FlyBase; FBgn0003891; tud. InterPro; IPR001097; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92038995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=7227;
                                                                                                                                                                  1062 QLKVGSTVVVRQRKDNAILRAT---VTACNHMMRKYRV----FCVDTGSLITVTSEDIWQ 1114
                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X62420; CAA44286.1; -. PIR; A41519; A41519.
                                                                                                                                                                                             108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             395 VPVIS
                                                                                  192
                                                                                                                                        164
                                                                                                                                                                                                                                                   58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OF COGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGION OF THE DEVELOPING COCYTE DURING THE EARLY TO MIDDLE STAGES
                                                                                                                                                                                                                                                 LDDSWIHPKNLTPS-----SPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASIL 107
                                                                                                                                                                                            YLE-GAELSVLQLNTNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVT---VHH 163
VQFD-YGNNVNFLCTYDDAKFVKSNPNLARRFKEFYE--GKSFALNVKNVCENNIVHLRP 1288
                                                                                                                                        LPKPIPDG----
                          VLLESFSDSENHSC-FDVVKQI-----FAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQP
                                                       NTSSTCSYTVNIFVNGASLRDMLVKAEFLTEVAPEIRVNLLAGQQIRGKFTSIRDMTSFK 1231
                                                                                  -MTTSC----VSSGSLWD-----
                                                                                                            LEQRFADPPCMAHRCSFHSVVTNYDPLY---IVDRMETFVPVNAKVDCEFVSKEKSNQGS
                                                                                                                                                                                                                                                                              l Similarity
77; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             399
                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=1936993;
                                                                                                                               -----DPNHKSKII-----FVP-----DCE-DSKMK-----
                                                                                                                                                                                                                                                                                           4.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                              50;
                                                                                                                                                                                                                                                                                           Score 87;
Pred. No.
                                                                                                                                                                                                                                                                              Pred. No. 41;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                 683C100AD308BADA CRC64;
                                                                                 ----PNITVETLDTQHLRVDFTLWNESTPYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2515
                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B
                                                                                                                                                                                                                                                                                119;
                                                                                                                                                                                                                                                                                                        Length 2515;
                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encodes
                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                  1171
                                                                                     231
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Q В

286

FFSSCLNDCLRHAVTVPCPVISNT-----TVPKPVADYI 319

1289

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RESULT 12
ICB4_HUADAN
ID 410EMAN
ID 210EMAH
AC P49662
DT 01-FEB
DT 01-FEB
DT 01-OCT
DE CASP4
OS PROTEA
GN CASP4
OS ENKARY
OC ENKARY
OC ENKARY
OC ENKARY
OC ENKARY
RA CO11ax
RA SU MA:
RY "A NON
RT "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "A novel human protease similar to the interleukin-1 beta converting enzyme induces apoptosis in transfected cells.";

EMBO J. 14:1914-1922(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Identification and characterization of ICH-2, a novel member interleukin-1 beta-converting enzyme family of cysteine protour. In 1961. Chem. 270:15250-15256(1995).

-i- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES CASPASE-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O1-FEB-1996 (Rel. 33, Created)
O1-FEB-1996 (Rel. 33, Last sequence update)
O1-OCT-2000 (Rel. 40, Last annotation update)
CASPASE-4 PRECURSOR (EC 3.4.22.-) (CASP-4) (ICH-2 PROTEASE) (TX PROTEASE) (ICE(REL)-II).
CASP4 OR ICH2.
                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Munday N.A., Vaillancourt J.P., Ali A., Casano F.J., Miller D.K., Molineaux S.M., Yamin T.-T., Yu V.L., Nicholson D.W.; Molineaux cloning and pro-apoptotic activity of ICErelII and ICErelIII, members of the ICE/CED-3 family of cysteine proteases."; Biol. Chem. 270:15870-15876(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-95262631; PubMed-7743998; Faucheu C., Diu A., Chan A.W.E., Blanchet Collard-Dutilleul V., Gu Y., Aldape R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                 or send an
                                                                                                     entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                         between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Terranova M., Ghayur T.;
"Identification and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bump N.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-95318091; PubMed=7797510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95318183; PubMed=7797592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., MUTAGENESIS OF C-258,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).
SIMILARITY).
TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH HIGHEST LEVELS IN
SPLEEN AND LUNG. MODERATE EXPRESSION IN HEART AND LIVER, LOW
SPLEEN AND LUNG. MODERATE EXPRESSION IN TESTIS. NOT FOUND IN THE
                                                                                                                                                                                                                                                                                                        CASPASE-11.
                                                                                                                                                                                                                                                                                                                                                           SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                        PTM: THE TWO SUBUNITS ARE DERIVED FROM THE PRECURSOR SEQUENCE AN AUTOCATALYTIC MECHANISM OR BY CLEAVAGE BY CASPASE-8.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                  CASPASE FAMILY.
                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced throu
  Z48810;
U28014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VMPLFMED--RRSFICPYPVVLSSFQALVVYTAKPYRVYV 1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J., Paskind M., Hugunin M., Talanian R.V., Allen H., Banach J., Hackett M.C., Johnston C.G., Li P., Mankovich J.A.,
                                                                                 email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                  THIS
  CAA88750.1;
AAA75171.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                            CONTAINS 1 CARD
IS PROTEIN COULD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                            DOMAIN.
BE THE HUMAN ORTHOLOG
                                                                                                                                                                                                                                             It is produced through
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                                                                                                                                                        There are no restrictions ng as its content is in
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                                                                                                                                  Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          novel member of the
                                                                                                                                       bу
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 29; Conserv
                                                                                                            REVISIONS.
Aberdam D.;
Submitted (1
                                                                                                                                                                                                 3B chain
J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    061789; Q61788; Q61966;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
LAMININ ALPHA-3 CHAIN PRECURSOR (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50209; CARD; 1.
PROSITE; PS01122; CASPASE_CYS; 1.
PROSITE; PS01121; CASPASE_HIS; 1.
PROSITE; PS50207; CASPASE_P10; 1.
PROSITE; PS50208; CASPASE_P20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00619; CARD; 1.
Pfam; PF00655; ICE_P10; 1.
Pfam; PF00656; ICE_P20; 1.
                      TISSUE=Lung;
MEDLINE=94281750; PubMed=8012114;
                                                                                                                                                                                                                                                              Galliano M.-F., Aberdam D., Aguzzi A., Ortonne J.-P., Mei
"Cloning and complete primary structure of the mouse lam.
                                                                                                                                                                                                                                                                                                       STRAIN=BALB/C; TISSUE=Lung; MEDLINE=95394948; PubMed=7665604;
                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00376; IL1BCENZYME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
    Aberdam D.,
                                                                 SEQUENCE OF 1052-1770 FROM
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAMA3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300 FIAFCSSTPHNV---SWRDSTMGSIF--ITQLIT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KPKVIIVQACRGA-----NRGELWVRDSPASLEVASSQSSENLEEDAVYKTHVEKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U25804; AAA86890.1;
P29466; 1IBC.
                                                                                                                                                                                                                                        Distinct expression pattern of the laminin alpha 3A and alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; IPR001309;
; IPR001315;
; IPR002138;
; IPR002398;
                                                                                                                                                                                                 isoforms.";
Chem. 270:21820-21826(1995).
                                                                                                              (APR-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thiol protease;
Galliano M.-F., Mattei M.-G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     781
271
290
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270
289
377
                                                                                                                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Veri
Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258 C->S: LOSS OF ACTIVITY.
43262 MW; DC7CCEC6E9D483EB CRC64;
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                                                                                                              the
                                                                   N.A.
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POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CASPASE-4 SUBUNIT :
POTENTIAL.
CASPASE-4 SUBUNIT :
CARD.
BY SIMILARITY.
                                                                                                              EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 86.5; Di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tation update)
(FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                   Vertebrata; I
thi; Muridae;
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    Pisani-Spadatora A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --- CFQKYSWCCH
                                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                       Murinae;
                                                                                                                                                                                                                                                                                       Meneguzzi
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6,

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InterPro; IPRO00034; -.
InterPro; IPR000501; -.
InterPro; IPR000501; -.
InterPro; IPR002049; -.
InterPro; IPR002049; -.
Pfam; PP00052; laminin_B; 1.
Pfam; PF00053; laminin_G; 3.
Pfam; PF00054; laminin_G; 3.
PROSITE; PS01128; EGF_1; 4.
PROSITE; PS01128; LAMININ_TYPE_EGF; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAME GENE. THE SEQUENCE SHOWN HERE IS THAT OF THE LARGER ISOFORM
B.
B.
TISSUE SPECIFICITY: BASAL MEMBRANE OF THE UPPER ALIMENTARY TRACT
AND URINARY AND NASAL EPITHBLIA, SALIVARY GLANDS AND TEETH (BOTH
VARLANTS). ISOFORM A IS PREDOMINANTLY EXPRESSED IN SKIN, HAIR
FOLLICLES AND DEVELOPING NEURONS OF THE TRIGEMINAL GANGLION.
ISOFORM B WAS FOUND IN BRONCHI, ALVEOLI, STOMACH, INTESTINAL
CRYPTS, WHISKER PADS, CNS, TELENCEPHALIC NEUROECTODERM, THALANUS,
RATEKE'S POUCH, AND PERIVENVIRICULAR SUBSPENDYMAL GERMINAL LAYER.
-1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
-1- SIMILARITY: CONTAINS 6.5 LAMININ BEGF-LIKE DOMAINS.
-1- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV (DOMAIN IV' IS NOT
SIMILAR TO LAMININ DOMAIN IV (DOMAINS).
-1- SIMILAR TO LAMININ DOMAIN IV (DOMAINS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Developmental expression of nicein adhesion protein (laminin-5) subunits suggests multiple morphogenic roles."; Cell Adhes. Commun. 2:115-129(1994).
                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mamm.
                                                                                                                                                      EMBL;
EMBL;
EMBL;
HSSP;
                                                                                                                                                                                                                                  entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Meneguzzi G
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                                                                                                                                            MGD;
                                                                                                                                                                                                                   tities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                          MGI:99909; Lama3.
                                                                                                                                                      X84014;
X84013;
L20478;
P02468;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OF 1052-1770 FROM
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of mouse nicein g
e 5:229-233(1994).
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                                                                                                                                                                   CAA58837.1;
CAA58836.1;
AAA68091.1;
                                                                                                                                                        1TLE.
Basement membrane; Extracellular matrix;
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              4.
 Coiled coil;
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SEQUENCE
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                                                                              CARBOHYD
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1557
1513
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1005
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591
1398
1500
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1600
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1819
  2569 AA;
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498
700
700
700
589
639
639
639
639
639
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969
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1057
1648
2569
1825
1994
2209
2385
22569
2385
2569
21964
1477
1477
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                                                                                                                      DOMAIN II AND I (HEPTAT REPEATS).

5 X LAMININ G-LIKE 1.

LAMININ G-LIKE 2.

LAMININ G-LIKE 3.

LAMININ G-LIKE 3.

LAMININ G-LIKE 4.

LAMININ G-LIKE 5.

COILED COIL (POTENTIAL).

BY SIMILARITY.

BY SIMI
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LAMININ EGF-LIKE 5.
LAMININ EGF-LIKE 6.
LAMININ EGF-LIKE 7 (
  MW;
                                                                   N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAMININ EGF-LIKE 1.
LAMININ EGF-LIKE 2.
LAMININ EGF-LIKE 4 (N-TERMINAL)
LAMININ DOMAIN IV (DOMAIN IV A)
3 X LAMININ EGF-LIKE REPEATS (D
                                                                                                    N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN III B.
3.5 X LAMININ
           MISSING (IN ISOFORM A).

MYVLPRLERLHIRGLHFTETQRLTLGEVGLEEASDTGSGPR
AHLVEMCACPPDYTGDSC -> MLPAVRWSAWSTGWLWIFG
AALGOCIGYGSEQQRVAFLQRPSQNHLQASYMELRPS (IN
ISOFORM A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN IV'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HEPTAT REPEATS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (C-TERMINAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEATS (DOMAIN
                                                                 (POTENTIAL).
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RESULT 14
DP3A_VIBCH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DP3A_VIBCH STANDARU;
P52022; Q9KPW7;
01-OCT-1996 (Rel. 34, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                         MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1960
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                                                                                                                                                                                  nature 406:477-483(2000).
-!- FUNCTION: DNA POLYMER
                                                                                                                                                                                                                  cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning and characterization of replicative DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-EL TOR INABA C6706 / SEROTYPE MEDLINE-97074886; PubMed-8917113;
                                                                                                                                                                                                                                                                                                                                                                             STRAIN=EL TOR N16961 / SEROTYPE 01;
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Franco A.A., Yeh P.E., Morris J.G. Jr.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2020 VPSLDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLED 2057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=666;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1840
                                                                                                                                                                                                                              DNA sequence of both chromosomes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                           FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN E RESPONSIBLE FOR MOST OF THE REPLICATIVE SYMPHESIS IN BATHIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5' EXONUCLEASE THE ALPHA CHAIN IS THE DNA POLYMERASE (BY SIMILARITY). CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE =
                              THETA CHAINS) THAT CAN REPAIR SHORT GAPS CREATED BY NUCLEY IN DUPLEX DNA. FOR EFFICIENT REPLICATION OF THE LONG, SING STRANDED TEMPLATES, POL III REQUIRES THE AUXILIARY CHAINS
                                                                               N PYROPHOSPHATE + DNA(N).
SUBUNIT: CONTAINS A CORE (COMPOSED OF ALPHA, EPSILON, AND
                                                                                                                                                                                                                                                                                                                                                                                                                            175:281-283(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERFPLSTPAFQGCMKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DGDP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGYARIPTQPNAPFPKLSWTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVKYKLNSEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGFELPRRLREPPYKGCIELDDLNENVLSLYNFKTTENLNTTEVEPCRRRKEESDKNYFE 1839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGRASPRLLDFPA-PYCAQ-EGLSCRV-----KNSTCLDDSWIHP-KNLTPSSPKNIYI 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proteobacteria;
                    AND
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   DELTA (BY SIMILARITY).
R LOCATION: CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----NHKSKIIFVPD-----CEDSKMKMTTSCVSSGSLWDPNIT 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -FLSMLQHHRKRWRFSFS-HFVVDPGQEYEVTVHHL---PKPIP 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Johnson J.A., Barry E.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLWNESTPYQVLLESFSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gamma subdivision; Vibrionaceae; Vibrio.
   CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 86; DB Pred. No. 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           of dnaE, encoding III, from Vibrio
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(BY SIMILARITY).
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                                                                                                                                                                                                                              cholera
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            cholerae
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                                                                                                                                                                                                                            pathogen Vibrio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          catalytic
                                                              BY NUCLEASE
                                                                                                                                                              IN BACTERIA
                                                                                                                                                                                ENZYME
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RESULT 15

DBL_HUMAN
ID DBL_HIM
AC P1091
DT 01-JU
DT 01-BP
DT 15-JU
DE PROTO
GN DBL O
OS Homo
OC Eukar
OC Mamma
OX NCBL
RN [1]
RP SEQUE
RC TISSU
RA ROn [
RT Oncog
RT NIH/;
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Best Local
                                                                                                                                                                                                   DBL_HUMAN STANDARD; PRT; 925 AA. P10911; P14919; O1-JUL-1989 (Rel. 11, Created) O1-APR-1990 (Rel. 14, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) PROTO-ONCOGENE DBL PRECURSOR [CONTAINS: MCF2]
MEDLINE-89052660; PubMed=3056717; Ron D., Tronick S.R., Aaronson S.A., Eva A.; "Molecular cloning and characterization of toncogene: evidence that its overexpression i NIH/3T3 cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                 TISSUE-Brain;
                                                                                             SEQUENCE FROM N.A.
                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                            DBL OR MCF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54 NSTCLDDSWIHPKNLTPSSPKNIYINLSVSSTQ---HGELVPVLHVEWTLQTDASILYLE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 LLLNVLAPGRASPRLLDFPAPVCAQEGL-----SCRVK-------
                                                                                                                                                                                                                                                                                                                                                                      TVRLGEY 281
                                                                                                                                                                                                                                                                                                                                                                                                  TFTLSKF 273
                                                                                                                                                                                                                                                                                                                                                                                                                                 IRVAIHDGYTLEDPRRPKNYSPKQYLRSEAEMC----ELFADIPEALANSVEIAKRCNV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGKSGEVGRALLKGNQQQVERCIEFYQTHFADHFYLELIRTGRAD-EESYLHFALDVAEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G---AELSVLQLNTNER---LCVKFQ-----FLSMLQHHRKRWRFSFSHFVVDPGQE 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KLTLLAKNNVGYKNLT------LLISKAYLRGHVQHQPVIDKAWLVEHAEGLIVLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 19.9
61; Conservative
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348 348 1 -> V (IN REF. 1).
348 348 1 -> V (IN REF. 1).
485 487 ALQ -> ELK (IN REF. 1).
685 685 7 -> P (IN REF. 1).
1000 1000 V -> A (IN REF. 1).
1103 1103 E -> G (IN REF. 1).
1117 1117 V -> A (IN REF. 1).
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19.9%;
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Primates;
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Pred. No. 21;
                                                                                                                                           Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EDAFE70BB830F293 CRC64;
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                  is
                the human dbl is sufficient
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              to tran
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EMBO J. 7:2465-2473(1988)

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EMBL; X12556; CAA31069.1; -
EMBL; J03639; AAA52172.1; A
EMBL; X13230; CAA31617.1; A
PIR; A30040; TVHUDB.
PIR; A28051; TVHUBD.
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REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was the support of the supp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -
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"A region of proto-dbl essential for its transforming activity sequence similarity to a yeast cell cycle gene, CDC24, and the breakpoint cluster gene, bcr.";
New Biol. 3:372-379(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 398-925 FROM N.A. MEDLINE=94167115; PubMed=2577874;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-88176886; PubMed=3281159;
Eva A., Vecchio G., Rao C.D., Tronick S.R.,
"The predicted DBL oncogene product defines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ron
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cellular transformation and guanine nucleotide exchange activity are catalyzed by a common domain on the dbl oncogene product.";
J. Biol. Chem. 269:62-65(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hart M.J., Eva A., Zangrilli D., Aaronson S.A., Evans T.,
Cerione R.A., Zheng Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHARACTERIZATION OF DBL DOMAIN. MEDLINE=94103281; PubMed=8276860;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oncogene 3:709-715(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl.
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PRINTS; PR00615; CCAATSUBUNTA.
PROSITE; PS00741; GDS_CDC24; 1
PROSITE; PS50003; PH_DOMAIN; 1
                                                                                                                                    InterPro; IPR000219; ...
InterPro; IPR000947; ...
InterPro; IPR001331; ...
InterPro; IPR001849; ...
                                                                                                                                                                                                                                                             MIM; 311030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 498-925 FROM N.A.
                                                                                  Pfam; PF00621; RhoGEF; 1.
                                                                                                            Pfam; PF00169; PH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY: EXPRESSED IN FETAL BRAIN AND ADRENAL GLANDS; IN THE ADULT, EXPRESSION IS LIMITED TO TESTES, OVARIES AND BRAIN. THE DH DOMAIN IS ESSENTIAL FOR TRANSFORMING ACTIVITY AND DIRECTLY CATALYZES GDP-GTP EXCHANGE ACTIVITY.

DISEASE: MCF. 2 AND DBL REPRESENT TWO ACTIVATED VERSIONS OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: CONTAINS 1 DBL-HOMOLOGY DOMAIN (DH). SIMILARITY: CONTAINS 1 PH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: PROMOTES THE EXCHANGE OF G25K-BOUND GDP BY GTP. A GUANINE NUCLEOTIDE EXCHANGE FACTOR FOR CDC42 AND RHOA, I FOR RACI AND TC10. CAN BE ACTIVATED BY TRUNCATION OF THE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAME PROTO-ONCOGENE
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                                                                                                                                                                                                                                                                                                                                            ALT_INIT.
ALT_SEQ.
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of amino-terminal coding
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MOD_RES
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CHAIN
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                                                                                                                                                                                                           MUTAGEN
                                                                         467
                                                                                           178 KIIFVPDCEDSKMKMTTSCVSSGSLWD---PNITVETLDTQHLRVDFTLWNESTPYQVLL 234
                  288
                                                      235
LERKDDFQMYA
                  SSCLNDCLRHA
                                    GYRAEMDNPEMFDLMPPLLRNKKDILFGNMAEIYEFHNDIF-LSSLENCAHAPERVGPCF
                                                     ESFSDSENHSCFDVV-----KQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFF
                                                                        KIEVVPDCQEKRSSGPSSSLDNGNSLDVLKNHVLNELIQTERVYV-----RELYTVLL
                                                                                                             1 Similarity 25.3
                                                                                                                                                           634
886
925 AA;
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398
498
498
687
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                  298
                                                                                                                                                            634 R
886 A
107657 MW;
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925
686
809
742
                                                                                                                       4.8%;
25.2%;
                                                                                                              22;
                                                                                                                       Score 85;
Pred. No.
                                                                                                                                                          DISSOCIATON.
R -> Q (IN REF. 4).
A -> V (IN REF. 3).
W; 0BCCB303275D19C9 CRC64;
                                                                                                                                                                                                                                                                            factor; Proto-oncogene; Phosphorylation;
                                                                                                                                                                                                 LLLKELL->IIIRDII: TRANSFORMATION CAPABILITY REDUCED; NO STIMULATION
                                                                                                                                                                                                                     PHOSPHORYLATION.
                                                                                                                                                                                                                                               MCF2 TRANSFORMING PROTEIN.
                                                                                                               Mismatches
                                                                                                                     DB
. 18;
                                                                                                                                 ۲,
                                                                                                                                 Length 925
                                                                                                                                                                                                   NO STIMULATION OF
                                                                                                               Indels
                                                                                                              18;
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                                     578
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Search completed: July 17, 2001, Job time: 158 sec 11:21:04

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Title:
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Maximum Match 100%
Listing first 45 summaries
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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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           TELEFAX: (206)
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, Milliam
TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
                                                                                                                                                                                                                                                                                                                                  COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5
SOFTWARE: Microsoft Word for Apple, Version
CURRENT APPLICATION DATA:
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                                                                            REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
                                                                                                                                       APPLICATION NUMBER: USSN 01
FILING DATE: 23 MARCH 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                        FILING DATE: 7 AUGUST 1995
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: USSN 08/620,694
FILING DATE: 21 MARCH 1996
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                                                                                                            NAME: Perkins, Patricia Anne REGISTRATION NUMBER: 34,695
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Best Local Similarity
Matches 322; Conserv
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0
CURRENT APPLICATION DATA:
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          ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
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PRIOR APPLICATION NUMBER:
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                                                                   APPLICATION NUMBER: FILING DATE: 23 MA
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Spriggs, Melanie
Fanslow, William
                                                                                                                                                                                                                                                                                                                                                                                    Immunex Corporation
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NUMBER:
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                                                                      USSN 08/410,535
CH 1995
                                                                                                                                                08/620,694
                                                                                                                                                                                                          us/09/022,696
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple PowerMacintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1
                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN
FILING DATE: 27 NOVEMBER
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Troutt, TITLE OF INVENTION:
                                 CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                                                                   CLASSIFICATION:
                                                                                                                                     APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                            COUNTRY: UZIP: 98101
                                                                                                                                                                                                                                                                                                                                           STREET:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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|VPCPVISNTTVPKPVADYIPLW 322
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51 University Street
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                                                                                  USSN 60/052,525
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                                                                    1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application Patent No. 6096305 GENERAL INFORMATION:
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Best Local Similarity
Matches 322; Conserv
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System
SOFTWARE: Microsoft Word for Apple, Versi
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
APPLICANT: Fanslow, William
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LENGTH: 864 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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FILING DATE: 21-MARC APPLICATION NUMBER: FILING DATE: 7 AUGU: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                         STREET: 51 Uni
CITY: Seattle
STATE: WA
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                                                                   APPLICATION NUMBER:
                                                                                                                          FILING DATE:
                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                  JMBER: US/08/620,694
21-MARCH-1996
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                                   USSN 08/538,765
                                                                                                                                           us/09/022,253
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Pred. No. 1.1e-183;
; Mismatches 0;
                                                                                                                                                                               Version
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PRIOR APPLICATION DATA: APPLICATION NUMBER:

USSN 08/410,535

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US-09-022-260-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: '706'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                          APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INTENTION: NO. 6100235el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
           COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                               STREET: 51 Uni
CITY: Seattle
STATE: WA
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TOPOLOGY: linear
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CLASSIFICATION:
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                                                                                                                98101
                                                                                                                                                                              51 University Street
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                                                                                                                                                                                               Immunex Corporation
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us/09/022,260
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                                                                                                                                                                                                                                   Sequence 2, Application US/09022259 Patent No. 6191104
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                                                                                                                                GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6191104el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
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NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 0:
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
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COMPUTER READABLE FORM:
                                                                                                                   CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid TOPOLOGY: linear
                 COUNTRY: USA
ZIP: 98101
                                                            ADDRESSEE: Immunex Corporation STREET: 51 University Street CITY: Seattle
                                                STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAIRRCWPRYVPGPALGWLLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60
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                                                                                                                                                       Sequence 2, Application US/09022257 Patent No. 6197525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 1766; DB 4; Best Local Similarity 100.0%; Pred. No. 1.1e-183; Matches 322; Conservative 0; Mismatches 0;
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                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Perkins, Patricia Anne REGISTRATION NUMBER: 34,695 REFERENCE/DOCKET NUMBER: 2617-B TELECOMMUNICATION INFORMATION: TELEPHONE: (206)587-0430
                  APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6197525el Receptor
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER:
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APPLICATION NUMBER:
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COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operatin
SOFTWARE: Microsoft Word for App
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CLASSIFICATION:
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Immunex Corporation
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
TYPE: amino acid
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating Sy
SOFTWARE: Microsoft Word for Apple,
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICATION NUMBER:
FILING DATE:
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TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180
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                                                          FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240
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Pred. No. 1.1e-183;
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; Sequence 10, Application US/08620694A
; Patent No. 5869286

GENERAL INFORMATION:

APPLICANT:

Yao, Zhengbin

US-08-620-694A-10

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APPLICANT:

Spriggs,

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US-08-620-694A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
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FILING DATE: 23 MARCH 1995
CLASSIFICATION: 435
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OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
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ZIP: 98101
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nes 230; Conserv
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               VPCPVISNTTVPKPVADYIPLW 322
                                                                                                        ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300
                                                                                                                                                           FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240
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                                                                                                                                                                                                                                                                                                            SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120
                                                                                                                                            LVPDCEHARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM
                                                                                                                                                                                                                  TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF
                                                                                                                                                                                                                                                                                       SWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
                                                                ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT
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William
No. 5869286el Receptor That Binds IL-17
                                                                                                                                                                                                                                                                                                                                                                                                                                  71.0%; Score 1254; DB 2;
71.4%; Pred. No. 7.3e-128;
70. Mismatches 60;
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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APPLICATION NOTICE OF APPLICATION NOTICE O
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operation
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: USSN 0
FILING DATE: 23 MARCH 1995
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
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                                                      241 ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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US-09-022-696-10
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Best Local Similarity
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
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LENGTH: 866 amino acids
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APPLICATION NUMBER: 1
FILING DATE: 23 MARCH
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                         TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 2617-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Perkins, Patricia Anne REGISTRATION NUMBER: 34,695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                                                                                                                                                                        1 MAIRRCWPRVVPGPALGWLLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60
                                 TNERLCVRFEELSKLRHHHRRWRFTFSHEVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS
                                                                THERLCYKFQFLSMLQHHRKRWRFSFSHFYVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180
                                                                                                   SWIHPRNUTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTLQTDASILYLEGAELSVLQLN 120
                                                                                                                                    SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120
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51 University Street
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23 MARCH 1995
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71.4%;
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Pred. No. 7
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US-08-978-773-4
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Best Local Similarity
Matches 230; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
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NAME: Perkins, Patricia
REGISTRATION NUMBER: 34,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for PowerMacintosh, Version
CURRENT APPLICATION DATA:
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MEDIM TYPE: Floppy disk
COMPUTER: Apple PowerMacIntosh
OPERATING SYSTEM: Apple Operati
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                                     121 TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF 180
                                                      121 TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180
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181 FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS 240
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                                                                                                                                                61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120
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                                                                                                                                                                                                         1 MAIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60
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51 University Street
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N: 530
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71.4%;
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Pred. No. 7.3e-128;
0; Mismatches 60;
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GENERAL INFORMATION:
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                                                                                                      Query Match
Best Local Similarity
Matches 230; Conserv
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APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17
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OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0
CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/9
FILING DATE: 21-MARCH-1996
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ATTORNEY/AGENT INFORMATION:
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301 VSCPEMPDT--PEPIPDYMPLW 320
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TOPOLOGY:
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61 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                 MAIRRCWPRVVPGPALGWLLLLLINVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD 60
                                    MGAARSPPSAVPGPLLGLLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD
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51 University Street
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23 MARCH 1995
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                                                                                                      71.0%; Score 1254; DB 3; 71.4%; Pred. No. 7.3e-128; ive 30; Mismatches 60;
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ST 1995
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                                                                                                                                      Length 866;
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US-09-022-260-10
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Patent No.
Query Match
Best Local Similarity
Matches 230; Conserv
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                                                                                                                                                                                   TELEFAX: (206)
INFORMATION FOR SEQ ID NO:
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APPLICANT:
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OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0
CURRENT APPLICATION DATA:
                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER:
FILING DATE: 23 MARC
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APPLICATION NUMBER:
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APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17
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                                                                                                                                                LENGTH: 866 amino acids
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                                                                                                                   TOPOLOGY:
                                                                                                                                    TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Seattle
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                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 34,695
                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                    TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
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 71.0%; Score 1254; I
71.4%; Pred. No. 7.30
tive 30; Mismatches
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 ; DB 3;
7.3e-128;
hes 60;
                                    Length 866;
     Indels
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     Gaps
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MGAARSPPSAVPGPLLGLLLLLGVLAPGGASLRLLDHRALVCSQPGLNCTVKNSTCLDD MAIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD

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Patent No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0
CURRENT APPLICATION NUMBER: US/09/022,259
                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                SEQUENCE CHARACTERISTICS
LENGTH: 866 amino acids
                                                                                                                                   NAME: Perkins, Patricia Anne
REGISTATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                  APPLICATION NUMBER: USSN FILING DATE: 23 MARCH 19 CLASSIFICATION: ATTORNEY/AGENT INFORMATION: NAME: DESCRIPTION DESCRIPTION
                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6191104el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
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301 VSCPEMPDT--PEPIPDYMPLW 320
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Best Local Similarity
301 VPCPVISNTTVPKPVADYIPLW 322
                                         241 ENHSCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT
                                                         241 ENHSCFDVVKQIFAPRQEEFHQRANVTETLSKFHWCCHHHVQVQPFFFSSCLNDCLRHAVT 300
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                                                                                                                                                                TNERLCVRFEFLSKLRHHHRRWRFTFSHFVVDPDQEYEVTVHHLPKPIPDGDPNHQSKNF
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                                                                                                                                                                                                                                                                                                                                                                     71.08;
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                                                                                                                                                                                                                                                                                                                                                                                   Length 866;
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240

Search completed: July 17, 2001, 11:19:22 Job time: 171 sec

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Title:
Perfect score:
Sequence:
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                        Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                July 17, 2001, 11:17:26; Search time 26.59 Seconds (without alignments) 922.460 Million cell updates/sec
                                                                                          US-09-488-728-2_COPY_1_322
1766
                                                                   1 MAIRRCWPRVVPGPALGWLL......CPVISNTTVPKPVADYIPLW 322
                                                                                                                                                                                                                                                                                                         GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Minimum DB seq length: 0
Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

219241

219241 seqs, 76174552 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir1:*
pir2:*
pir3:*
pir4:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	σ	. UI	4	ω	2	1	No.	Result
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H		DNA polymerase III		posterior-group pr	leukotriene-B4 20-	l poly		hypothetical prote	coronin-like prote	protein-tyrosine-p	ucan 1,	gamma-		T16G12.1 protein -		.	vacuolar protein s	hypothetical prote	granulocyte/macrop	gamma-aminobutyric	protein-tyrosine k	probable membrane	GABAA receptor del	gamma-aminobutyric	integumentary muci	\mathbf{c}	e transc	ase-related p	Description	

ALIGNMENTS

F;1967-1975/Region: protein kinase ATP-binding motif F;49,65,77,123,132,265,287,307,333,377,480,607,628,706,714,911,940,962,971,1110,1154,

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ent) #status predicted
F;1996/Active site: Lys #status predicted
F;2127,2131,2132/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation)
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A; Map
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R;Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, February 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable transcription activator [imported] - fission yeast (Schizosaccharomyces
C; Species: Schizosaccharomyces pombe
C; Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: Z25032
A; Accession: T50064
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A; Residues: 1-708 <HAR>
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                                                                                                                                                                                                                   44 AQEGLSCRVKNSTCL------DDSWIHPKNLTPSSPKNIYINL------SV
                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNKLFLTDIDSNHTIWEVLTNRNIKDICYTADDDKVYYI--LEDSLFLLNVQSTSESQLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDVFLRNVTAITVDWIARHLFVAMKTSWNETQVFFIDLELKTKS-----LKALNIQLGKR 1281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----IPDGDPNH-----
                                                                                          KFQFLSMLQHHRK-RWRFSFSHFVVDPGQEYEVTVHHLPKPI-----PDGDPNHKSKII 180
                                                                                                                          ASQDVKSDGTLPIGTNNNPLIPSHSQESSHWTIRHESMPSALAGSSAQSMQ---
                                                                                                                                                                                       AQPNLCIPCSLGTCLIHFHEFSSSSFMDPVSLFCSSP---YPNLPPHSRSSSLESKKPSV
                                                                                                                                                      SS-----TQHGELVPVLHVE---WTLQTDASILYLEGAELSVLQLNTNERLCV 127
SDLSYEEFLKKYSSTKVERVSEAAPPPSSLNSSTVLDENDSLISQGSSVDDQ----TDFLG
                               ----FVPDCEDSKMKMTT---
                                                             --QFPSITQNEENFRFKKSFTQ-
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Pred. No. 0.77;
15; Mismatches 127
                                                                                                                                                                                                                                                                     Score 112.5; I
Pred. No. 0.19;
                               ---SCVSSGSLWDPNITV----ETLDTQHLRVDFTL 223
                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                   DB
                                                              -PQPIVKETTFPKSEPGQEHAKL
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C;Superfamily: protein-tyrosine kinase axl; fibronectin type III repeat homology; C;Keywords: ATP; glycoprotein; growth factor receptor; phosphotransferase; transfo c;1-31/Domain: (or 7-31) signal sequence #status predicted <SIG>F;32-880/product: (or 32-874) protein-tyrosine kinase tyro3 #status predicted <MATF;50-109/Domain: immunoglobulin homology <IMM1>F;50-109/Domain: immunoglobulin homology <IMM2>F;146-195/Domain: fibronectin type III repeat homology <FN3B>F;312-395/Domain: fibronectin type III repeat homology <FN3B>F;419-441/Domain: transmembrane #status predicted <IMM>F;419-441/Domain: transmembrane #status predicted <IMMP
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Neuron 6, 691-704, 1991
A; Title: An extended family
A; Reference number: PT0183;
A; Accession: PT0185.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;514-522/Region: protein kinase ATP-binding motif
F;515-766/Domain: cytoplasmic tyrosine kinase #status predicted <CTK>
F;53,75,181,220,230,283,356,370/Binding site: carbohydrate (Asn) (cov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: brain A; Note: It is uncertain whether Met-1 or Met-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-880 <OHA>
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A; Residues: 650-703 <LAI>
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C;Comment: This receptor plays an important role in development, function,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAIRRCWPRVVPGPALGWLLL--LLNVLAPGRASP--RLLDFPAPVCAQEG----LSCRV
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                                                                                                                                                   PPEPVTIFWWRGPTKVGGPASSPSVLNVTGVTQRTEFSCEAHNIKGLATSRPAIIRLQAP
                                                                                                                                                                                                                       QEYEVTVHHLPKPIPDGDPNHKSKIIFVP-----DCEDSKMK-MTTSCVSSGSLWDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGMDDPDIHWMKDGAVVQNASQ---VSISISEQ---NWIGLLSLKSAERSDAGLYWCQVK 110
PAAPFNITVTTISSSNASV---AWVPGADGLALL--
                                                                       ----NITVETLDTQHLRVDFTLWNESTPYQVLLESFSDSENHSCFDVVKQIFAPRQEEF
                                                                                                                                                                                                                                                                                                                                                                                            ELSVLQLNTNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDP-----
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Pred. No. 2.2;
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    -HSC--TVQVAHAP--GEW
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A;Cross-references: GB:M60587; GB:M60588; GB:M60589; GB:M60591; GB:M60592; GB:M60593; GE:C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor: transmembrane nrotein
                                                                                                                                 C;Accession: A36303
R;Sommer, B.; Poustka, A.; Spurr, N.K.; Seeburg, P.H.
DNA Cell Biol. 9, 561-568, 1990
A;Title: The murine GABA-A receptor delta-subunit gene:
A;Reference number: A36303; MUID:91103876
A;Accession: A36303
                                                                                                                                                                                                                                                                   gamma-aminobutyric acid receptor A delta chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #te
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C; Superfamilv:
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C;Species: Xenopus laevis (African clawed frog)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 03-Nov-2000
                                                               A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-449 <SOM>
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J. Biol. Chem. 272, 1805-1810, 1997
A;Title: Similarities of integumentary mucin B.1 (FIM-B.1)
A;Reference number: Z20920; MUID:97153143
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A; Residues: 1-1506 < JOB>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                               252 IFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLN-DCLRHAVTVP-CPVISN 308
:|| :| :| :| :| :| :| :| 586
696 LFANQQCSQLKDPNGAFAK-----CHSTVLYRSFYERCVHLTCISQDMTVSMCTELRN 748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 TCLDDSWIHPKNLTPSSPK---NIYINL--SVSSTQHGELVPV--LHVEW------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDSENHSCFDVVKQ 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THLHVNLLIQTGTTMQFYTSVPSTGYEDTEG-----PCGSFNHKADDDFM-----SNQK 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QHHRKRWRF----SFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKIIFVPDCEDSKMK 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DWVP
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Similarity 21.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -PESSPETF-----VGF--WK-----MSSCSDPVKPTCIDLEKE 695
receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VPVPPF -- TCLLRNLAPATNYSLRVRC --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35; Mismatches 110;
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Pred. No. 5.
                                                                                                                                                                                                                                                                      28-Mar-1991 #text_change
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GABAA receptor delta subunit - mouse
C; Species: Mus sp. (mouse)
C; Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_cha
C; Caccession: 152630
R; Wang, J.B.; Kofuji, P.; Burt, D.R.
Brain Res. Bull. 29, 119-133, 1992
A; Title: Strain comparisons and developmental profile of the A; Reference number: 152630; MUID:92370453
A; Accession: 152630
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-449 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:S42882; NID:g253879; PIDN:AAB22967.1; PID:g253880 C;Superfamily: acetylcholine receptor C;Keywords: neurotransmitter receptor
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    183
                                                                                                                                                         102 YNHTNETLGLDSRFVDKL-----WLPDTFIVNAKSAWFHDVTVENKLIRLQPDG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 ---VILY-----SIRITSTVAC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102
                                                                              151 ---VILY-----SIRITSTVAC-----DMDLAKYPLDEQECMLD--
                                                                                                                                                                                                                                                                         64
                                                                                                                                                                                                                                                                                                                                                  16 LGWLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKN-----STCLDDSWI-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 LGWLLLLUVLAPGRASPRLLDFPAPVCAQEGLSCRVKN-----STCLDDSWI-----
                                                                                                                                                                                                                                                                   ---HPKNLTP---SSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HKSKIIFVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLL 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YNHTNETLGLDSRFYDKL------WLPDTFIVNAKSAWFHDYTVENKLIRLQPDG---
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ESY----GYSSEDIV-YYWSENQEQIHGLDRLQLAQFTITSYRF
                                      ESFSDSENHSCFDVVKQIFAPRQEEFH-----QRANVTFTLSKF 273
                                                                                                              HKSKIIFVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLL 234
                                                                                                                                                                             QLNTNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQE--YEVTVHH-LPKPIPDGDPN 174
                                                                                                                                                                                                                                 MEGYARNFRPGIGGAPVNVALALEVASIDH --- ISEANMEYTMTV --- FLHQSWRDSRLS 101
                                                                                                                                                                                                                                                                                                            LGWILL-----PLLL-----LCTQPHHGARAMNDIGDYVGSNLEISWLPNLDGL 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESY----GYSSEDIV-YYWSENQEQIHGLDRLQLAQFTITSYRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESFSDSENHSCFDVVKQIFAPRQEEFH-----QRANVTFTLSKF 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEGYARNFRPGIGGAPVNVALALEVASIDH----ISEANMEYTMTV---FLHQSWRDSRLS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGWLLL-----PLLL-----LCTQPHHGARAMNDIGDYVGSNLEISWLPNLDGL 47
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22.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                            Score 99; DB 2; Length 449; Pred. No. 1.4;
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RESULT S63127

probable membrane protein YNL172w - yeast (Saccharomyces N;Alternate names: hypothetical protein N1677

cerevisiae)

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C;Species: Saccharomyces cerevisiae
C;Date: 27-Apr-1996 #sequence_revis
C;Accession: S63127
                                                                                                                                                                                                                                                                                                              C;Species: Mus musculus (house mouse)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 18-Jun-1999
C;Accession: B53743; 344141; JC2146; 149198; 149151; 148863; 148860
R;Mark, M.R.; Scadden, D.T.; Wang, Z.; Gu, Q.; Goddard, A.; Godowski, P.J.
J. Biol. Chem. 269, 10720-10728, 1994
J. Biol. Chem. 269, 10720-10728, 1994
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A;Residues: 1-1748 <OBE>
A;Cross-references: EMBL:Z71448; NID:g1302143; PID:e239542; PID:g1302144; MIPS:YNL172W
                                                                                                                                                                                                                                                              J. Biol. Chem. 269, 10720-10728, 1994
A;Title: rse, a novel receptor-type tyrosine kinase with homology to Axl/Ufo,
A:Reference number: A53743; MUID:94193774
                                                                                                                                                                                                                                                                                                                                                                                                                                         protein-tyrosine kinase (EC 2.7.1.112) tyro3 precursor - mouse N; Alternate names: protein-tyrosine kinase sky; receptor-type tyrosine kinase
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F;1382-1398/Domain: transmembrane #status predicted <TM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: 14L
C;Keywords: transmembrane protein
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A; Molecule
                                           A; Reference number: S44141
A; Accession: S44141
                                                                                                               submitted to the EMBL Data Library, March 1994
                                                                                                                                       A;Cross-references: GB:U05683; NID:g469518; R;Lai, C.; Gore, M.; Lemke, G.
                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-880 < MAR>
                                                                                                                                                                                                                                 A;Status: preliminary
                                                                                                                                                                                                                                                    A; Accession: B53743
                                                                                           A;Description:
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                        Status:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 TQHGELVPV-----LHVEWTLQTDASILYLEGAELSVLQLN-----TNERL---CVKFQ 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 GRASPRILDFPAP-VCAQEGLSC---RVKNSTCLDDSWIHPKNLTPSSPKNIYINLSVSS 84
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                                                                                       Structure, expression and activity of TYRO3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENLKLKEPSRIQAMYIHELLESCLILVSEGQNKEEYKACLYDPFVKI-TSPS
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Sequence Database, April 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---QHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKS 177
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22.9%;
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                                                                                                                                                               PIDN: AAA19237.1;
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A;Residues: 7-629,'R',631-810,'V',812-880 <LAI>
A;Cross-references: EMBL:X78103; NID:g473096; PIDN:CAA54995.1; PID:g473097
R;POlV1, A; Armstrong, E; Lai, C.; Lemke, G.; Huebner, K.; Spritz, R.A.; Guida, Gene 134, 289-293, 1993
A;Title: The human TYRO3 gene and pseudogene are located in chromosome 15q14-q25.
A;Reference number: JC2145; MUID:94085793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Superfamily: protein-tyrosine kinase axl; fibronectin type III repeat hom C; Keywords: ATP; 91/coprotein; growth factor receptor; phosphotransferase; F;1-31/Domain: (or 7-31) signal sequence #status predicted <SIG>F;32-880/Product: protein-tyrosine kinase tyro3 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:U23721; NID:g901992; PIDN:AAC52217.1; R;Lai, C.; Gore, M.; Lemke, G. Oncogene 9, 2567-2578, 1994
A;Title: Structure, expression, and activity of Tyro 3, a neural A;Reference number: I48860; MUID:94336210
A;Accession: I48860
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A;Cross-references: EMBL:U18933; NID:g622982; PIDN:AAC52148.1; PID:g622983
R;Schulz, N.T.; Paulhiac, C.I.; Lee, L.; Zhou, R.
Brain Res. Mol. Brain Res. 28, 273-280, 1995
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R; Crosier, P.S.; Lewis, P.M.; Hall, L.R.; Vitas, M.R.;
Growth Factors 11, 125-136, 1994
Qy
                                                                                                                                                                                                                                                                                                               F;514-522/Region: protein kinase ATP-binding motif
F;515-766/Domain: cytoplasmic tyrosine kinase #status predicted <CTK>
F;53,75,181,220,230,283,356,370/Binding site: carbohydrate (Asn) (cov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;146-195/Domain: immunoglobulin homology <IMM2>F;214-299/Domain: fibronectin type III repeat homology F;313-395/Domain: fibronectin type III repeat homology F;313-395/Domain: transmembrane #status predicted <TMM>F;419-441/Domain: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Identification of alternative exons, including A;Reference number: I48861; MUID:95303487 A;Accession: I48863
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A; Residues: 7-629, 'R', 631-810, 'V', 812-880
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A; Residues: 1-92 < RE3>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;506-783/Domain:
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                                                                                                                                              Query Match
Best Local :
                                                                                                      Matches
    1 MAIRRC--WPRVVPGPALGWLLL--LLNVLAPGRASP--RLLDFPAPVCAQEG----LSC
                                                                                                                                     Similarity
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Pred.
                                                                                                      Mismatches
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No.
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A;Cross-references: GB:X69986
R;Shivers, B.D.; Killisch, I.; Sprengel, R.; Sontheimer, H.; Koehler, M.; Schofield, P.F.
Neuron 3, 327-337, 1989
A;Title: Two novel GABA-A receptor subunits exist in distinct neuronal subpopulations.
A;Reference number: JQ0076; MUID:90380375
A;Recession: JQ0076
A;Molecule type: mRNA
A;Residues: 1-92, RA, 95-130, 'VCIV', 135-403, 'VP', 406-449 <SHI>
A;Residues: 1-92, RA, p5-130, 'VCIV', 135-403, 'VP', 406-449 <SHI>
A;Experimental source: brain
C;Comment: Neurotransmission effected by gamma-aminobutyric acid (GABA) is mediated main
C;Comment: The GABA-A receptor consists of subunits that are structurally related to lig
C;Superfamily: acetylcholine receptor
C;Keywords: 91ycoprotein; neurotransmitter receptor; transmembrane protein
F;17-449/Product: gamma-aminobutyric acid A receptor delta chain #status predicted <TMI>
F;275-297/Domain: transmembrane #status predicted <TMI>
F;275-297/Do
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                                                                                                                                                            F;309-331/Domain: transmembrane #status predicted <TM3>
F;427-449/Domain: transmembrane #status predicted <TM4>
F;103,106/Binding site: carbohydrate (Asn) (covalent) #status
F;164-178/Disulfide bonds: #status predicted
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R;Motejlek, K.; Haeuselmann, R.; Leitgeb, S.; Luescher, B.
J. Biol. Chem. 269, 15265-15273, 1994
A;Title: BSF1, a novel brain-specific DNA-binding protein recognizing a tandemly repeate
A;Reference number: A53811; MUID:94253091
A;Accession: A53811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-26 <MOT>
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A; Status: prelimina
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A; Title: Isolation of distantly related members in a multigene
A; Reference number: A34625; MUID:90179746
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Query Match
Best Local Similarity
Matches 63; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Residues: 1-449 <ZHA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YGDWVP 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPAAPFNTTVTTISSYNASV---AWVPGADGLALL-----HSC--TVQVAHAP--G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VGPPEPVTIYWWRGLTKVGGPAPSPSVLNVTGVTQRTEFSCEARNIKGLATSRPAIVRLQ
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   Conservative
                             5.4%;
   44;
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                             Score 95; I
Pred. No. 3;
   Mismatches
                                                                   DB
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85;
                                                                   Length 449;
Indels
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Gaps
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C;Accession: A45304
C;Accession: A45304
R; Bartin, U.; Sorensen, R.; Luhr, S.; Morrissey, P.J.; Cosman, D.; Larsen Proc. Natl. Acad. Sci. U.S.A. 89, 4295-4299, 1992
A;Title: Cloning of the low-affinity murine granulocyte-macrophage colony-stimulating A;Reference number: A45304; MUID:92262426
A;Accession: A45304; MUID:92262426
A;Accession: A45304
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-388 <PAR>
A;Residues: 1-388 <PAR>
A;Cross-references: GB:M85078; NID:g192594; PIDN:AAA37421.1; PID:g192595
A;Cross-references: GB:M85078; NID:g192594; PIDN:AAA37421.1; PID:g192595
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151
                                                                                                                                                                                                                                                                                                                                                                                     50 CRVKNSTCLDDSWIHPKNLTPSSPKNIYINLSV-SSTQH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                  88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 ---HPKNLTP---SSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16
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VTCRRFEVTRRLFPP
                          ENHSCEDVVKQIFAP 255
                                                                                  ---RAGDTRMK-----HWGEWSPAHPLEAEDT---RVPGALLYAVTACAVLLCALALG
                                                                                                                           FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS
                                                                                                                                                                     SWAPPSTWASLTARDFQFEVQWQSAEPGSTPRKVLVVEETRLAFPSPAPHG--GHKVKV-
                                                                                                                                                                                                                  RW----
                                                                                                                                                                                                                                                          IANDLSLL----GSEAYLVVTGRSGAGPVRFLDDVVATKALERLGPPRDVTASCNSSHCTV
                                                                                                                                                                                                                                                                                                  LQTDASILYLEGAELSVLQLNTNERLCVKF-----QFLSML------
                                                                                                                                                                                                                                                                                                                                             CEIRAARFLSCAW----REGPAAPADVRYSLRVLNSTGHDVARCMADPGDDV----ITQC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                  RCWFRRMMALHHGVTLDVNGTVGGAAAHWRLSFVNESAAGSGA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESFSDSENHSCFDVVKQIFAPRQEEFH-----QRANVTFTLSKF 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---VILY-----SIRITSTVAC------DMDLAKYPMDEQECMLD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HKSKIIFVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEGYARNFRPGIGGPPVNVALALEVASIDH---ISEANMEYTMTV---FLHQSWRDSRLS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGWLLL--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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21.6%;
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                                                                                                                                                                                                             RESESHEVVDPGQE----YEVTVHHLPKPIPDGDPNHKSKII 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 94; I
Pred. No. 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ---- ENLT
                                                                                                                                                                                                                                                                                                     -QHHRK 140
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hypothetical protein AAG10824.1 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

G86300

RESULT

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C; Accession: G86300

C; Accession: G86300

R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C. A.; Li, J.H.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, C. C. A.; Li, J.H.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Reference number: A86141; MUID:21016719

A;Accession: G86300

A;Accession: G86300
                                                                                                               A; Notacus, Francis DNA
A; Molecule type: DNA
A; Residues: 1-3131 < PUR>
A; Cross-references: EMBL:AL021767; PIDN:CAA16910.1; GSPDB:GN00067; SPDB:SPBC16C6.02c
A:Fxperimental source: strain 972h-; cosmid c16C6
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A; Residues: 1-682 <STO>
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                                                                                                                                                                                                                                                                           C;Accession: T39553
R;Purnelle, B.; Goffeau, A.; Wood, V.; Lyne, submitted to the EMBL Data Library, February
                                                                                                                                                                                                                                                                                                                                    C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-pec-1999
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                                                                      A; Map position: 2
A; Introns: 8/1; 45/3; 96/3; 2958/3
                                                                                                                                                                                                                                                                                                                                                                           vacuolar protein sorting-associated protein - fission
                                                                                                                                                                                                                                          A; Reference number: Z21863
A; Accession: T39553
                                                                                                           A; Gene: SPDB: SPBC16C6.02c
                                                                                                                                                                                                                      A; Status: preliminary; translated from GB/EMBL/DDBJ
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l Similarity 22.9%;
71; Conservative
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5.2%;
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Pred. No.
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Score
Pred.
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No. 68;
                                                                                                                                                                                                                                                                                   M.; Barrell, B.G.; Rajandream,
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                   Length
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R;Ainscough, R.
R;Ainscough, R.
submitted to the EMBL Data Library,
submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein Y44A6C.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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T26891
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A; Introns: 6/2; 155/3
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A; Residues: 1-333 <WIL>
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A;Experimental source: clone Y44A6C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary; translated from
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260 KIADHFYPDQED--
                                                                                                                                                                                                      147 SHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKIIFV--PDCEDSKMKMTTSCVSSGS---
                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                           50 CRVKNSTCLD---
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                                      VVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAV 299
                                                                                  RLQILSIQGNSWQNYWDPSDVLEGLNAE---
                                                                                                                                                                  KMFQLD----YLSVTHSDWMVPSDLEEMENKIVYLDKSDFYDSDMNQFLRELKSGSSHS
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                                                                                                                         ---LWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDSENHSCFD
                                                                                                                                                                                                                                                                                                                                                                                                                                       5.2%; Score 91; DB 2; 20.2%; Pred. No. 4.5;
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    -GFGAELEHGVDLSEAFDFLKNDGTRVSV
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                                                                                    -LWNQTERNQ---HYFLNAEHRKNFK
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A;Introns: 49/3; 79/2; 188/1; 205/2; 273/3; 338/1; 432/3; 515/3; 585/1; 616/3; 733/2; 77
C;Superfamily: membrane alanyl aminopeptidase
                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, February 1994 A; Reference number: S42837 A; Accession: S42841
                                                                                                                                                                                                                                                                                                                                                                                                   T16G12.1 protein - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Feb-1995 #sequence_revision 20 C;Accession: S42841
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A;Molecule type: DNA
A;Residues: 1-885 <THO>
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C;Keywords: microtubule
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A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type; mRNA
A;Residues: 1-606 <SMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R:Smith, E.; Lefebvre, P.
submitted to the EMBL Data Library, November 1996
A;Description: The PP20 gene product contains WD repeats and localizes to the inter-micr
A;Reference number: Z16400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Chlamydomonas reinhardtii
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C;Accession: T08180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:U78547; NID:g1813637; PID:g1813638
                                                                                                                                                                                                                           A; Cross-references: EMBL: Z30317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF20 protein, microtubule-associated – Chlamydomonas reinhardtii
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Matches 61; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      393 KIWDFEKQRCV----TTFTDHKQAIWSVRF------HHLGEVVASGSLDHT 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   283 VSAGPRSGW----ASLNAPPRRNPYADLEFPAAPVKMLSLNKTFKGHL-----LSVANL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 FA 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            491 YGHQNSCNGVSFNILGTQLASTDADGVVKLWDTRMTAEVATINTGKHPANKSCFDRSGQV 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  434 VRLWDLP---AGKCRMALRGHVDSVNDLAWQPFSSSLATASSDKTVSVWDARAGLCTQTY 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 333 ALHPTKPILVTASDDKTWKMWHMPGGDLIMCGEGHKDWVAGVDFHPAGTCLASGGGDSAV 392
  28 PGRASPRLLDFP--
                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 VVPGPALGWLLLLLNVLAPGRASPRL-LDEPAPVCAQEGLSCRVKNSTCLDDSWIHPKNL 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPSSPKNIYINLSVSST-----QHGELVPV--LHVEWTLQTD----ASILYLEGAELSV 116
                                                                 Similarity
                                              Conservative
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                                                                 21.2%;
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20.2%; Pred. No. 13;
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                                       Score 89.5; DB 2;
Pred. No. 20;
4; Mismatches 108;
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--- APVCAQEGLSCRVKNSTCLDDSWIHP 65
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719 VSKFQW 724
                                          270 LSKFHW 275
                                                                                     664 EMTKFLDLTLYLVNEDSLAPWEQAIEFFTEMLNR--FQYQPEIDTVRNYVIQITKN---A 718
                                                                                                                                                                              604 LPTGYRVDNAGSTSFARINYDDKSWYSIQAQLLSNMNTMSSTTRAMLLDDANFFYQSGRW
                                                                                                                                                                                                                         168 IPDG-------DPNHKSKIIFVPDCE-DSKMKMTTSCVSSGSLWDPNITVETLDT 214
                                                                                                                                                                                                                                                                        559 Q--ANQOSCMSDETL------WNVPLFTQTPGALDENWFVNFTGGNDATWL----RP
                                                                                                                                                                                                                                                                                                                                                              499 YGYVNASPRNLWTSLTVAAQRHNITDWNGQPLDVSSFMDPYTLQTSYPIITLTLRGTSTV 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                           450 PGVAKPVISDTPPVFGIEPYYKGSALLNLLNNVLTPAVFQEGLS---
                                                                                                                                215 QHLR-VDFTLW--NEST--PYQVLLESFSDSENHSCFDVVKQIFAPRQEEFHQRANVTFT
                                                                                                                                                                                                                                                                                                                                                                                                           KNLTPSSPKNIYINLSVSSTQH-----GELVPVLHV--EWTLQTDASILYLEGAELSVL 117
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Search completed: July 17, 2001, 11:19:56 Job time: 150 sec

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Result
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Maximum DB seq length: 2000000000
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1 MAIRRCWPRVVPGPALGWLL......CPVISNTTVPKPVADYIPLW 322
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                                                                                                            Mouse interleukin-
Murine IL-17R prot
Murine IL-17R prot
Murine interleukin
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Soluble IL-17R/Fla
Murine interleukin
                                                         Murine
                              Murine
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IL-17R poly
Interleukin
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interleukin
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84	84.5	84.5	86	86.5	86.5	86.5	86.5	86.5	88	88	88	88	92	95.5	97	137	208.5	208.5	282.5	282.5	282.5	282.5	282.5	282.5	1254	1254	1254	1254	1254	1254	1254	1254	1254
4.8	4.0	. 60	4.9	4.9	4.9	4.9	4.9	4.9	5.0	5.0	5.0	5.0	5.2	5.4	ហ ហ	7.8	11.8	11.8	16.0		16.0	16.0	16.0	16.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0
452	565	340	322	377	377	377	377	377	993.	874	874	874	729	977	880	34	385	385	502	433	433	426	426	426	866	866	866	866	866	866	866	866	866
17	16	21	20	20	17	17	17	16	σ	20	19	15	21	22	16	20	22	21	22	21	21	21	21	21	22	22	21	21	21	21	20	19	17
AAR97299	AAR/6700	AAB03643	AAY14072	AAY21718	AAR90702	AAW00213	AAR88750	AAR84740	AAP50116	AAW81402	AAW79145	AAR60545	AAY44857	AAB31164	AAR77846	AAY39426	AAB75381	AAB25795	AAB87604	AAY70595	AAB18754	AAY49946	AAY70591	AAB18750	AAY72754	AAB62066	AAB03807	AAY97181	AAY97131	AAY99941	AAW92409	AAW61272	AAW04185
Human GABA-A recep	EIET enterotoxin e	Rat IgE heavy chai	~	Amino acid sequenc	Interleukin-1-beta	Human Ich-2 protei	Human Tx protease,	Interleukin-1-beta	O	Receptor protein t	Receptor protein t	Murine development	Mouse taste cell s	Amino acid sequenc	Mouse Rse rPTK. M	_		Human secreted pro	Human PRO5801. Ho	Interleukin 17-lik	A human interleuki	Human interleukin	Interleukin 17-lik	S)	Interle			Human interleukin	interl	IL-17R	Human IL-17R prote	-	Human interleukin-

ALIGNMENTS

04-DEC-2000 (first entry)

Soluble IL-17R/Flag fusion protein.

AAY97255;

AAY97255 standard; peptide;

330

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RESULT
AAY97255
ID AAY9
XX AAY9
AC AAY9
DT 04-I
XX Solt
XX IL-1
KW IL-1
KW HSVJ
KW ANCJ
KW ANCJ
KW ANCJ
KW HSVJ
KW HSVJ
KW ET Prot
FT Prot
FT Prot
FT Prot
FT Pep
FT Pep
FT Pop
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Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IL-17R; interleukin-17 receptor; soluble; CTIA-8; Herpesvirus saimiri; HSV13; graft rejection; suppressor; immunosuppressive; anti-allergic; anti-asthmatic; Flag epitope; fusion protein.
21-MAR-1996;
23-MAR-1995;
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96US-0620694.
95US-0410535.
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                                                                                                                                                                                                                                                                                                                                                                                                                        /label= IL-17_receptor_extracellular_domain 323...330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Signal_peptide
32..322
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1..322
                                                                                                                                                                                                                                                                                                                                                                    /label= Flag_epitope
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Murine

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RESULT
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AC AAY9
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AC AAY9
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AC AAY9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Suppressing rejection of a grafted syngeneic or allogeneic organ tissue in a graft recipient for organ transplantation involves transfecting the organ or tissue with DNA encoding soluble interleukin-17R receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                  asthma and autoimmune diseases. Note: This sequence does not appear in the specification. from the full length murine IL-17R (see AAY97180) and the (see AAY97183)
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  04-DEC-2000
                      AAY97258;
                                         AAY97258 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                        VPCPVISNTTVPKPVADYIPLW 322
                                                                                                                                         enhscfdvvkqifaprqeefhqranvtftlskfhwcchhhvqvqpffssclndclrhavt
                                                                                                                                                                                TNERLCYKFQFLSMLQHHRKRWRFSFSHFYVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180
                                                                                                                                                                                                                                                                     swihpknltpsspkniyinlsvsstqhgelvpvlhvewtlqtdasilylegaelsvlqln
                                                                                                                                                                                                                                                                                 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN
                                                                                               vpcpvisnttvpkpvadyiplw
                                                                                                                                                             ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT
                                                                                                                                                                                                                            tnerlcvkfqflsmlqhhrkrwrfsfshfvvdpgqeyevtvhhlpkpipdgdpnhkskii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Column -; 27pp;
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                                                                                                                                                                                                                                                                                                                                                          100.0%; ilarity 100.0%; Conservative 0
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                    Score 1766; DB 21; Pred. No. 2.2e-169;
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23-MAR-1995;
07-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                             immune or inflammatory response in a mammal comprises administering soluble IL-17R. Soluble II-17R fragments comprise residues I-320 of the murine IL-17R, residues I-320 of the human IL-17R, and fragments of the extracellular domain that bind IL-17. The method is useful for regulating an immunoresponse, for treating or preventing diseases like allergy, asthma and autolimmune diseases, and for suppressing rejection of grafted organs or tissues in the recipient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A novel interleukin-17 receptor (IL-17R) was identified by screening cDNA library from T cell thymnoma EL4 cells, which were identified as binding fusion proteins comprising human immunoglobulin G1 (IgG1) Fc region and soluble IL-17 (CTLA-8) protein or a homologous Herpesvirus saimiri (HSV) protein, designated HSV13. Regulating an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Regulating, treating or preventing immune or inflammatory response mammal, especially organ or graft rejection, allergy or asthma, comprises administering interleukin-17 receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US6100235-A
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                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Column -; 27pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-FEB-1998;
                                                                                                                                                                                                                 Local Similarity
                                                                                       This sequence does not appear in the specification. the full length murine IL-17R (see AAY97130) and the AAY97132)
swihpknltpsspkniyinlsvsstqhgelvpvlhvewtlqtdasilylegaelsvlqln
                        SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ωC,
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                                                                                                                                                                                                                                                                                                                330 AA;
                                                                                                                                                                                     100.0%; Score 1766; DB 21; ilarity 100.0%; Pred. No. 2.2e-169; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spriggs MK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-0620694.
95US-0410535.
95US-0538765.
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                                                                                                                                                                                                                                          DB 21;
                                                                                                                                                                                             Indels
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RESULT
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                  The murine interleukin-17 receptor (IL-17R) (AAW04184) is a type I transmembrane protein that binds IL-17 (CTLA-8, see also AAW02386) and HVS13 (AAW02387), a viral homologue of IL-17. Its amino acid sequence was deduced from a cDNA clone (AAY33800) isolated from murine thymoma EL4 cells. Soluble, recombinant forms of the receptor (partic. amino acids 1-322) can be prepd. in transformed host cells and used to regulate immune and inflammatory responses, in methods for suppressing rejection of grafted organs or tissue, and in assays of IL-17 and IL-17R.
                                                                                                                                                                                                                                                                                                                                                                                                                         Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW04184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW04184 standard;
 Sequence
                                                                                                                      Claim 1; Page 29-32; 52pp; English.
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23-MAR-1995;
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asthma; graft rejection;
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DB; AAT33800.
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950S-0410535
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32..322
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                                                                                                                                                                                                       MX,
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                                                                                                                                                                                                                                                                                                                                       Cytoplasmic_tail
                                                                                                                                                                                                                                                                                                                                                                                                                                                             IL-17R; autoimmune disease; allergy;
inflammation; cytokine; therapy.
                                                                                                                                                                                                       Yao
                                                                                                                                          receptor - useful for regulating immune or to suppress graft rejection
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RESULT AAW61271 ID WAW61271 ID AAW61271 ID AAW6 1271 MAW Cart KW Inter KW Cart KW Cart KW Cart FT Prot FT Prot FT Prot FT Doma FT Doma
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Best Local Similarity
Matches 322; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interleukin-17 receptor; IL-17 receptor; mouse; nitric oxide;
cartilage; osteoarthritis; autoimmune disease; inflammation;
                                          (IMMV ) IMMUNEX CORP
                                                                                                27-NOV-1996;
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ilarity 100.0%;
Conservative (
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                                                                                                                                               97WO-US21451.
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/note= "Claim 2(a)"
                                                                                                                                                                                                                                                                                                                                                                                     'label= Extracellular
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                                                                                                                                                                                                                                                                                                                                      label= Transmembrane
                                                                                                                                                                                                                                                                                       Extracellular
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Pred. No. 8.6e-169;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This polypeptide comprises mouse full-length interleukin-17 creeptor (IL-17R). A claimed method for reducing the amount of nitric oxide produced by a cartilage associated cell comprises contacting the cell with a soluble IL-17R, especially claimed soluble murine or human (see AAW61272) IL-17R comprising the signal peptide and extracellular domains of the respective full-length receptors. Recombinant soluble IL-17R polypeptides can be obtained using prokaryotic or eukaryotic (for glycosylated products) expression systems. A cDNA sequence (see AAW27591) coding for full-length murine IL-17R is provided. IL-17 is known to stimulate nitric oxide production from cartilage-associated cells in individuals with osteoarthritis. Inhibitors of nitric oxide production, such as soluble IL-17R, may therefore be useful to ameliorate the effects of nitric oxide in osteoarthritis as in other disease conditions in which nitric oxide plays a role, e.g. autoimmune and inflammatory diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 322; Conser
IL-17R; murine; interleukin-17 receptor; immunoregulator; inhibitor; T cell proliferation; T cell activation; organ; graft; rejection; autoimmune disease; allergy; astima; treatment; inflammatory disease B cell proliferation; immunoglobulin secretion; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2(a);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contacting cells with soluble interleukin-17 receptor, useful treat osteoarthritis and autoimmune and inflammatory diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reducing nitric oxide production by cartilage associated cells contacting cells with soluble interleukin-17 receptor, useful t
                                                                                                                                                      AAW92408 standard; Protein;
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llarity 100.0%;
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Pred. No. 8.6e-169;
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Best Local
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23-MAR-1995;
07-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                      This sequence represents a murine interleukin-17 receptor (IL-17R). IL-17R polypeptides have immunoregulatory activity. They can be used inhibiting T cell proliferation, or for inhibiting T cell activation. particular they can be used for preventing or treating organ or graft rejection, autoimmune disease, allergy or asthma. They can also be use for the prevention or treatment of inflammatory disease in which activated T cells play a role or for inhibiting B cell proliferation or immunoglobulin secretion. The IL-17 polypeptides can also be used as immunogens, reagents in in vitro assays, or as binding agents for
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                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                   ENHSCEDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT
                                                                                                                                vpcpvisnttvpkpvadyiplw
                    VPCPVISNTTVPKPVADYIPLW 322
                                         enhscfdvvkqifaprqeefhqranvtftlskfhwcchhhvqvqpffssclndclrhavt
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                                                                                                                                                                                                                                                                                                                                               purification procedures.
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95US-0410535
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32..864
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 322
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Pred. No. 8.6e-169;
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Matches 322;
           Query Match
Best Local Similarity
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23-MAR-1995;
07-AUG-1995;
                                                                                 The present invention relates to a novel receptor that binds Interleukin 17 (IL-17, also known as CTLA-8) and a Herpesvirus saimiri homolog, HVS13. The receptor is a type I transmembrane protein which is referred to as IL-17R. Murine thymona EL4 cells were found to express a receptor for IL-17. An EL4 mammalian expression library was screened and a cDNA encoding the receptor was identified. The present sequence is the murine IL-7R protein. The cDNA was used to isolate DNA encoding human IL-17R by cross species hybridisation. The human IL-17R cDNA and protein are described in AAA61240 and AAY99941. Soluble forms of the receptor may be used to regulate immune responses, for example to suppress rejection of organ grafts. Antibodies to IL-17R consisting of amino acids 1-322 of murine IL-17R or 1-320 of human IL-17R may be useful as components of diagnostic or research assays. Such antibodies may also be used in affinity purification of the receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IL-17R;
murine;
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                                                             864
Conservative
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95US-0410535.
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32..864
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                                                                   21-MAR-1996;
23-MAR-1995;
07-AUG-1995;
                                                                                                                                                                                                                                                                                                IL-17R; interleukin-17 receptor; soluble; CTLA-8; Herpesvirus saimiri; HSV13; graft rejection; suppressor; immunosuppressive; anti-allergic; anti-asthmatic.
                 WPI; 2000-548298/50
                                                                                                                                                                   Domain
         N-PSDB; AAA51987.
                                 Fanslow
                                                                                                      11-FEB-1998;
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                                 Spriggs
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95US-0410535.
95US-0538765.
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32..864
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1..322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              binding fusion proteins comprising human immunoglobulin G1 (IgG1) FC region and soluble IL-17 (CTLA-8) protein or a homologous Herpesvirus saimiri (HSV) protein, designated HSV13. Regulating an immune or inflammatory response in a mammal comprises administering soluble IL-17R. Soluble IL-17R fragments comprise residues 1-322 of the murine IL-17R, residues 1-320 of the human IL-17R, and fragments of the extracellular domain that bind IL-17. The method is useful for regulating an immunoresponse, for treating or preventing diseases like allergy, asthma and autoimmune diseases, and for suppressing rejection of grafted organs or tissues in the recipient.
                                               Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Regulating, treating or preventing immune or inflammatory response mammal, especially organ or graft rejection, allergy or asthma, comprises administering interleukin-17 receptors
                  Peptide
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                                                                                              HSV13;
                                                                                                      IL-17R;
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                                                                                                                                                                                                                                                                                                                                              vel interleukin–17 receptor (IL-17R) was identified by screening library from T cell thymoma EL4 cells, which were identified as
                                                                                                                                                                                                                                        VPCPVISNTTVPKPVADYIPLW 322
                                                                                                                                                                                                                                                                              ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT
                                                                                                                                                                                                                                                                                                                   FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS
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                                                                                                                                                                                                                               vpcpvisnttvpkpvadyiplw
                                                                                            graft
                                                                                                                          interleukin-17
                                                                                            interleukin-17 receptor; soluble; CTLA-8; Herpesvirus saimiri;
graft rejection; suppressor; immunosuppressive; anti-allergic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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/label=
32..864
                                              Location/Qualifiers
                           /label= Soluble_IL-17_receptor
                                                                                                                        receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAR-1996;
23-MAR-1995;
07-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A novel interleukin-17 receptor (IL-17R) was identified by screening cDNA library from T cell thymoma EL4 cells, which were identified as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Suppressing rejection of a grafted syngeneic or allogeneic organ tissue in a graft recipient for organ transplantation involves transfecting the organ or tissue with DNA encoding soluble interleukin-17R receptor
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95US-0410535.
95US-0538765.
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323..34
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32..322
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23-MAR-1995;
07-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to an isolated and purified interleukin-17 receptor (IL-17R). A soluble IL-17 protein (OTLA8) and a herpesvirus siamiri (HVSI3) open reading frame (homologous to CTLA8) were expressed as fusion proteins comprising an immunoglobulin Fc region, and used to screen for the expression of the IL-17R. The screening identified the novel receptor of the invention. IL-17R is a type I transmembrane protein that exhibits antiinflammatory, immunosuppressive, antiasthmatic and antiallergic activities, and is an inhibitor of T cell proliferation and activation. IL-17R can be used to regulate immune functions, and is useful for preventing or treating organ or graft rejection, autoimmune disease, allergy or asthma. The present sequence represents the murine interleukin-17 receptor amino acid sequence identified in the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interleukin-17 receptor protein useful for regulating immune functions and for preventing or treating organ or graft rejection, autoimmune disease, allergy or asthma in human -
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22; Conservative
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95US-0410535.
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rejection; graft rejection; autoimmune disease
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23-MAR-1995;
07-AUG-1995;
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                                                                                                                                                                                New assay kits for detecting interleukin-17 (IL-17), IL-17 receptors and (antagonists or mimetics of) the interaction between IL-17 and IL-17 receptor, useful for treating autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                Yao Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-FEB-1998;
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                                                                                                                                          Claim 1;
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DB; AAF57186.
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                                                                                                                                                                                                                                                                                                                                                Spriggs MK,
                                                                                                                                        Columns 19-26;
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95US-0410535.
95US-0538765.
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323..3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "mature protein"
                                                                                                                                     26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          864
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The invention is directed towards assays for detection of interleukin-17 (IL-17), IL-17 receptor (IL-17R), and (antagonists or mimetics of) the interaction between IL-17 and IL-17R. The assay kit comprises an IL-17R protein and a detecting reagent. The method is useful for inhibiting binding of IL-17 to cells expressing IL-17R. IL-17 receptors are also

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RESULT 1
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Best Local :
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                                                                                                                                                                        Key
                                                                                         Domain
                                                                                                          Domain
                                                                                                                                              Protein
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                                                                                                                                                                                                                                                                                                   AAY72748 standard; Protein;
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21-MAR-1996;
23-MAR-1995;
                                                              US6191104-B1
                                                                                                                            Domain
                                                                                                                                                               Peptide
                                                                                                                                                                                                           inflammatory
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                          11-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                    TNERLCYKFQFLSMLQHHKKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180
                                                                                                                                                                                                                                                                                                                                                        VPCPVISNTTVPKPVADYIPLW 322
                                                                                                                                                                                                                                                                                                                                                                                 SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120
                                                                                                                                                                                                                                                                                                                                               vpcpvisnttvpkpvadyiplw
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322; Conser
                                                                                                                                                                                                                                              Interleukin-17
                                                                                                                                                                                                         Interleukin-17 receptor; IL-17R; immunosuppressive; antiallergic; matic; antiinflammatory; graft rejection; autoimmune disease; atory disease; allergy; CTLA-8; immunogen; asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  864
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96US-0620694
95US-0410535
                           98US-0022259
                                                                                                                                    1..31
/label= Signal_peptide
32..864
32..864
                                                                                                                            /label 32..32
                                                                                                                                                                       Location/Qualifiers
                                                                                                                  /label= Extracellular_domain
                                                                                                 /label= Transmembrane_domain
                                                                                                                                                                                                                                              receptor (IL-17R) or CTLA-8
                                                                                                                                   _= Mature_murine_IL-17_receptor
                                                                               Cytoplasmic_tail
                                                                                                                                                                                                                                                                                                    864
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Pred. No. 8.6e-169;
; Mismatches 0;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interleukin-17 and their corresponding nucleic acid molecules. IL-17R is a Type I transmembrane protein which is used for regulating the immune response. The invention is useful for suppressing rejection of a grafted organ or tissue in a graft recipient. Soluble IL-17 (CTLA-8) receptors are useful for preventing or treating organ or graft rejection, autoimmune disease, allergy, asthma, and inflammatory disease in which activated T-cells play a role. Soluble IL-17 fusion proteins are used to screen cells for the expression of IL-17 receptor. Derivatives of IL-17R are also used as immunogens, reagents in in vitro assays, or as binding agents for affinity purification procedures.
Interleukin-17 receptor;
asthma; graft rejection;
                                        Human interleukin-17 receptor.
                                                                                              AAW04185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to Interleukin-17 receptors (IL-17R)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTLA-8 receptor.
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                                                                   05-DEC-1996
                                                                                                                       AAW04185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             present sequence is murine Interleukin-17 receptor
                                                                                                                                                                                                     VPCPVISNTTVPKPVADYIPLW 322
                                                                                                                                                                                                                                                                                               TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180
                                                                                                                                                                                                                                                                                                                                                                                                                        SWIHPKNLTPSSPKNIYINLSVSSTQHGELVPVLHVEWTLQTDASILYLEGAELSVLQLN 120
                                                                                                                                                                                                                                                             ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFFSSCLNDCLRHAVT
                                                                                                                                                                                                                                                                                                                                                                                                            swihpknltpsspkniyinlsvsstqhgelvpvlhvewtlqtdasilylegaelsvlqln
                                                                                                                                                                                          vpcpvisnttvpkpvadyiplw
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                                                                                                                                                                                                                                                                                                                                                      tnerlcvkfqflsmlqhhrkrwrfsfshfvvdpqqeyevtvhhlpkpipdqdpnhkskii
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                                                                                                                         standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        864 AA;
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                                                                                                                         Protein;
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               IL-17R; autoimmune disease;
                                                                                                                         866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1766; DB 22;
Pred. No. 8.6e-169;
; Mismatches 0;
 cytokine;
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                allergy;
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                                                                                                                                                                                                                                                                                                                                         The human interleukin-17 receptor (IL-17R) (AAW04184) is a type I transmembrane protein. Its amino acid sequence was deduced from a cDNA clone (AAM3801) isolated from a human peripheral blood lymphocyte library. Soluble, recombinant forms of the receptor (partic. amino acids 1-320) can be prepd. in transformed host cells and used to regulate immune and inflammatory responses, in methods for suppressing rejection of grafted organs or tissue, and in assays of IL-17 and IL-17R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-AUG-1995;
23-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
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                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              encoding interleukin-17 receptor - useful for regulating immune inflammatory responses, or to suppress graft rejection
            VPCPVISNTTVPKPVADYIPLW 322
                                       | | | : : | |: | : | | 320
                                                     ENHSCFDVVKQIFAPRQEEFHQRANVTFTLSKFHWCCHHHVQVQPFFSSCLNDCLRHAVT
                                                                                                FVPDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNESTPYQVLLESFSDS
                                                                                                                              TNERLCVKFQFLSMLQHHRKRWRFSFSHFVVDPGQEYEVTVHHLPKPIPDGDPNHKSKII 180
                                                                                                                                                                                                                                           MAIRRCWPRVVPGPALGWLLLLLNVLAPGRASPRLLDFPAPVCAQEGLSCRVKNSTCLDD
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95US-0410535.
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342..866
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AAW61272
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                                  This polypeptide comprises human full-length interleukin-17 receptor (IL-17R). A claimed method for reducing the amount of nitric oxide produced by a cartilage associated cell comprises contacting the cell with a soluble IL-17R, especially claimed soluble interpretation of the respectation of the signal peptide and extracellular domains of the respective full-length receptors. Recombinant soluble IL-17R polypeptides can be obtained using prokaryotic or eukaryotic (for glycosylated products) expression systems. A cDNA sequence coding for full-length human IL-17R is provided (see AAV27592). IL-17 is known to stimulate nitric oxide production from cartilage-associated cells in individuals with osteoarthritis. Inhibitors of nitric oxide production, such as soluble IL-17R, may therefore be useful to ameliorate the effects of nitric oxide in osteoarthritis as well as in other disease conditions in which nitric oxide plays a role,
                                                                                                                                                                                                                                                                                                                Reducing nitric oxide production by cartilage associated cells -contacting cells with soluble interleukin-17 receptor, useful to treat osteoarthritis and autoimmune and inflammatory diseases
                          e.g. autoimmune and
                                                                                                                                                                                                                                                                                  Claim 2(b); Page 27-31; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-322457/28.
N-PSDB; AAV27592.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-NOV-1997;
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cartilage; osteoarthritis; autoimmune disease; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human interleukin-17 receptor
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/note= "Claim 2(b)"
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                             inflammatory diseases.
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Best Local S
Matches 230
                                                                                         21-MAR-1996;
23-MAR-1995;
07-AUG-1995;
                                                                                                                                                                                                Key
Peptide
                                                                                                                                                                                                                                       IL-17R; human; interleukin-17 receptor; immunoregulator; inhibitor; T cell proliferation; T cell activation; organ; graft; rejection; autoimmune disease; allergy; asthma; treatment; inflammatory disease; B cell proliferation; immunoglobulin secretion; immunogen.
Isolated interleukin-17 receptor DNA - used to develop products for treating e.g. organ or graft rejection, autoimmune disease, allergy asthma or inflammatory disease
                                                                                                                                          09-FEB-1999
                                                                                                                                                        US5869286-A.
                                                                                                                                                                                 Protein
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                                 N-PSDB;
                                          WPI;
                                                         Fanslow
                                                                         (IMMV ) IMMUNEX CORP
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nes 230; Conserv
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DB; AAX01922.
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vscpempdt--pepipdymplw 320
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                                                                                        96US-0620694.
95US-0410535.
95US-0538765.
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28..866
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                                                                                                                                                                                        signal_peptide
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RESULT 15
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                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         affinity purification procedures.
                              Protein
                                                                                        Domain
                                                                                                                      Domain
                                                                                                                                                 Peptide
                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                         IL-17R; CTLA-8; interleukin 17; Herpesvirus saimiri; HVS
murine; antibody; immune suppression.
                                                                                                                                                                                                                                                                    Human IL-17R protein
                                                                                                                                                                                                                                                                                                 10-JAN-2001 ·
                                                                                                                                                                                                                                                                                                                               AAY99941;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enhscfehmhhipaprpeefhqrsnvtltlrnlkgccrhqvqiqpffssclndclrhsat
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342..866
                             /label= Cytoplasmic_domain
32..866
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                                                                                                                                                                 Location/Qualifiers
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71.4%;
                IL-17R
                                                                        Transmembrane_domain
                                                                                                     Extracellular_domain
                                                                                                                                  Signal_peptide
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Pred. No. 2.8e-117;
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23-MAR-1995;
07-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a novel receptor that binds Interleukin 17 (II-17, also known as CTLA-8) and a Herpesvirus saimiri homolog, HVS13. The receptor is a type I transmembrane protein which is referred to as IL-17R. Murine thymona EL4 cells were found to express a receptor for IL-17. An EL4 mammalian expression library was screened and a cDNA encoding the receptor was identified. The murine IL-17R cDNA and protein are described in AAA61238 and AAY99935. The CDNA was used to isolate DNA encoding human IL-17R by cross species hybridisation. The present sequence is the human IL-7R protein. Soluble forms of the receptor may be used to regulate immune responses, for example to suppress rejection of organ grafts. Antibodies to IL-17R consisting of amino acids 1-322 of murine IL-17R or 1-320 of human IL-17R may be useful as components of diagnostic or research assays. Such antibodies may also be used in affinity purification of the receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US6072037-A
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibodies immunoreactive with interleukin-17 receptor protein useful in interfering with receptor binding to CTLA-8, as components of diagnostic or research assays or in affinity purification of the receptor -
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N-PSDB; AAA61240.
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mes 230; Conserv
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                                                     enhscfehmhhipaprpeefhgrsnvtltlrnlkgccrhqvqiqpffssclndclrhsat 300
                                                                                                                                                                                                                                                                                                                                                                                                                      866 AA;
                                                                                                                                                                                                                                                                                                                                              71.0%; Score 1254; DB 21; ilarity 71.4%; Pred. No. 2.8e-117; Conservative 30; Mismatches 60;
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95US-0410535.
95US-0538765.
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